OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: February 10, 2005, 11:21:18 ; Search time 3299 Seconds
               (without alignments)
               1662.808 Million cell updates/sec

Title: US-10-659-782A-32
Perfect score: 616
Sequence: 1 MPSPGTVCSLLLGMLWLDL........PPSSRERSRRSHQPSCSPEL 116

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext 0.5
               Ygapop 10.0 , Ygapext 0.5
               Fgapop 6.0 , Fgapext 7.0
               Delop   6.0 , Delext 7.0

Searched: 4526729 seqs, 2364484745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10659782/runat_05022005_161917_4270/app_query.fasta_1.263
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10659782 @CGN_1_1_3731 @runat 05022005 161917 4270 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Database : GenEmbl:*
            1: gb_ba:*
            2: gb_htg:*
            3: gb_in:*
            4: gb_om:*
            5: gb_ov:*
            6: gb_pat:*
            7: gb_ph:*
            8: gb_pl:*
            9: gb_pr:*
           10: gb_ro:*
           11: gb_sts:*
           12: gb_sy:*
           13: gb_un:*
           14: gb_vi:*

Result No.	Score	% Match	Query Length	DB	ID	Description
1	605.5	98.3	507	11	G72347	G72347 ghrelin X1-
2	605.5	98.3	5199	9	AF296558	AF296558 Homo sapi
c 3	605.5	98.3	104947	9	AC008116	AC008116 Homo sapi
4	605.5	98.3	146947	2	AC012515	AC012515 Homo sapi
c 5	605.5	605.5	98.3	210053	9 AC022384	AC022384 Homo sapi
c 6	605.5	605.5	98.3	216292	2 AC012600	AC012600 Homo sapi
c 7	605.5	605.5	98.3	217778	9 AC090841	AC090841 Homo sapi
8	500.5		81.2	6008	9 AY372274	AY372274 Macaca mu
9	220.5		35.8	362	4 AY455990	AY455990S1 Cervus el
10	214.5		34.8	354	4 AY455987	AY455987 Odocoileu
11	214		34.7	351	6 AR170496	AR170496 Sequence
12	214		34.7	351	6 AR208181	AR208181 Sequence
13	214		34.7	351	6 AR404108	AR404108 Sequence
14	214		34.7	351	6 AX062356	AX062356 Sequence
15	214		34.7	351	6 AX154581	AX154581 Sequence
16	214		34.7	351	6 BD061161	BD061161 Motilin h
17	214		34.7	402	9 AY184207	AY184207 Homo sapi
18	214		34.7	511	6 CQ722673	CQ722673 Sequence
19	214		34.7	511	6 CQ794618	CQ794618 Sequence
20	214		34.7	511	6 BD012137	BD012137 Novel pep
21	214		34.7	511	9 AB029434	AB029434 Homo sapi
22	214		34.7	519	9 AJ252278	HSA252278 Homo sapi
23	214		34.7	526	6 BD222667	BD222667 Human sig
24	214		34.7	527	6 AX356127	AX356127 Sequence
25	214		34.7	542	9 BC025791	BC025791 Homo sapi
26	214		34.7	654	6 AR252557	AR252557 Sequence
27	214		34.7	654	6 AX403380	AX403380 Sequence
28	214		34.7	654	6 AX464308	AX464308 Sequence
29	214		34.7	654	9 AY359053	AY359053 Homo sapi
30	212.5		34.5	362	4 AY455994	AY455994S1 Odocoileu
31	209.5		34.0	362	4 AY455988	AY455988S1 Rangifer
32	208.5		33.8	479	9 AB035700	AB035700 Homo sapi
33	208.5		33.6	508	9 BD012139	BD012139 Novel pep
34	207		33.6	354	9 AY371699	AY371699 Macaca mu
35	205		33.3	410	4 AY422043	AY422043S1 Sus scrof
36	203		33.0	233811	10 AC117596	AC117596 Mus muscu
37	197.5		32.1	4513	10 AB060078	AB060078 Mus muscu
38	194		31.5	643	4 AB089201	AB089201 Felis cat
39	192.5		31.2	362	4 AY455985	AY455985S1 Capra hir
40	192.5		31.2	640	4 AB089202	AB089202 Felis cat
41	190		30.8	366	4 AY455979	AY455979S1 Bos tauru
42	190		30.8	366	4 AY455981	AY455981S1 Kogia bre
43	180		29.2	324	4 AY455992	AY455992S1 Alces alc
44	178		28.9	366	4 AY454076	AY454076S1 Bison bis
45	178		28.9	487	6 CQ794617	CQ794617 Sequence

ALIGNMENTS

RESULT 1
G72347
LOCUS   G72347   507 bp   DNA   linear   STS 20-JUN-2001
DEFINITION ghrelin X1-2 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION   G72347
VERSION   G72347.1 GI:14518296
KEYWORDS   STS.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 507)
AUTHORS   Cox,D.G., Boillot,C. and Canzian,F.
TITLE   Genome Survey
JOURNAL   Unpublished (2000)
COMMENT   Contact: Federico Canzian
            Genome Analysis Group
            International Agency for Research on Cancer
            150, cours Albert-Thomas, F-69372 Lyon Cedex 08 France
            Tel: +33-4-72738698
            Fax: +33-4-72738388
            Email: canzian@iarc.fr
            Primer A: AGACCCTCTCTCCCCAG
            Primer B: TCCTCGCTGCCACAGAAG
            STS size: 507
            Protocol:
            Template: 50   ng

```
        Primer:           4         uM each
        dNTPs:            2         mM each
        MgCl2:            1.5-2.5   mM
        Taq:              0.05      units
        Total Vol:        25        ul

        Buffer:
        MgCl2:            1.5-2.5   mM
        KCl:              50 mM
        Tris-HCl:         20 mM
        pH:                         8.4.

FEATURES         Location/Qualifiers
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                 /organism="Homo sapiens"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:9606"
                 /clone_lib="Human"
     STS         1..507
     primer_bind 1..18
     primer_bind complement(490..507)
ORIGIN

Alignment Scores:
Pred. No.:          9.89e-43        Length:          507
Score:              605.50          Matches:         116
Percent Similarity: 99.15%          Conservative:    0
Best Local Similarity: 99.15%       Mismatches:      0
Query Match:        98.30%          Indels:          1
DB:                 11              Gaps:            1
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US-10-659-782A-32 (1-116) x G72347 (1-507)

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Qy    1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   48 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG 107

Qy   21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  108 GCCATGGCAGGCTTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 167

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  168 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCGTGACCTGGAG 227

Qy   61 GlnGlnArgHis---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
          ||||||||||        |||||||||||||||||||||||||||||||||||||||
Db  228 CAGCAGCGCCATCTCGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 287

Qy   80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 99
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  288 CTCACTGTTTCTGGAAGGACATGGGGGTTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 347

Qy  100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  348 AGCAGAGAAAGGAGTGCGAAGAAGCCACCAGAAGCCAAGCTGCAGCCCGAGCTC 398
```

RESULT 2
AF296558
LOCUS   AF296558   5199 bp   DNA   linear   PRI 02-OCT-2000
DEFINITION Homo sapiens growth hormone secretagogue precursor (GHRELIN) gene,
            complete cds.
ACCESSION   AF296558
VERSION   AF296558.1 GI:9966512
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 5199)
  AUTHORS   Wajnrajch,M.P., Ten,I.S., Gertner,J.M. and Leibel,R.L.
  TITLE   Genomic Organization of the human GHRELIN gene
  JOURNAL   J. Endocr. Genet. 1, 231-233 (2000)
REFERENCE   2 (bases 1 to 5199)

AUTHORS   Wajnrajch,M.P., Ten,I.S., Gertner,J.M. and Leibel,R.L.
TITLE   Direct Submission
JOURNAL   Submitted (15-AUG-2000) Pediatrics, Weill Medical College of
          Cornell University, 525 East 68th Street, Room M-624, New York, NY
          10021, USA

FEATURES   Location/Qualifiers
     source   1..5199
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                 /mol_type="genomic DNA"
                 /db_xref="taxon:9606"
                 /chromosome="3"
                 /map="3p26-p25"
                 /clone="BAC CTB-187P1"
     gene   1..5199
                 /gene="GHRELIN"
                 /note="GHS"
     mRNA   join(1..554,749..865,3814..3922,4732..5199)
                 /gene="GHRELIN"
                 /product="growth hormone secretagogue precursor"
     exon   1..554
                 /gene="GHRELIN"
                 /number=1
     5'UTR   1..446
                 /gene="GHRELIN"
     CDS   join(447..554,749..865,3814..3922,4732..4751)
                 /gene="GHRELIN"
                 /codon_start=1
                 /product="growth hormone secretagogue precursor"
                 /protein_id="AAG10300.1"
                 /db_xref="GI:9966513"
                 /translation="MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP
                 PAKLQPRALAGWLRPEDGQAEGAEBDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFL
                 QDILWEEAKEAPADK"
     mat_peptide join(516..554,749..793)
                 /gene="GHRELIN"
                 /product="growth hormone secretagogue"
     misc_feature 522..524
                 /gene="GHRELIN"
                 /note="octanoylation; modified site"
     intron   555..748
                 /gene="GHRELIN"
                 /number=1
     exon   749..865
                 /gene="GHRELIN"
                 /number=2
     intron   752..865
                 /gene="GHRELIN"
                 /note="alternative"
                 /number=2
     intron   866..3813
                 /gene="GHRELIN"
                 /number=2
     exon   3814..3922
                 /gene="GHRELIN"
                 /number=3
     intron   3923..4731
                 /gene="GHRELIN"
                 /number=3
     exon   4732..5199
                 /gene="GHRELIN"
                 /number=4
     3'UTR   4752..5199
                 /gene="GHRELIN"
ORIGIN

Alignment Scores:
Pred. No.:   1.02e-41   Length: 5199
Score: 605.50   Matches: 116
Percent Similarity: 99.15%   Conservative: 0
Best Local Similarity: 99.15%   Mismatches: 0
Query Match: 98.30%   Indels: 1
DB: 9   Gaps: 1

```
US-10-659-782A-32 (1-116) x AF296558 (1-5199)

Qy     1  MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu  20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   447  ATGCCCTCCCCAGGAACCGTCTGCAGCCTCTTCCTGCTCGGCATGCTCTGGCTGGACCTG  506

Qy    21  AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro  40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   507  GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC  566

Qy    41  HisLysAlaProHisValArgProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   567  CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG  626

Qy    61  GlnGlnArgHis---TrpPheSerGlnThrLysAspSerGlySerAsp  79
          ||||||||||   ||||||||||||||||||||||||||||||
Db   627  CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGACCACAAAGGACTCTGGGTCTGAC  686

Qy    80  LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer  99
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   687  CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCTAAACAGACTGTTTCCCCTTCC  746

Qy   100  SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu  116
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   747  AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC  797


RESULT 3
AC008116/c
LOCUS       AC008116       104947 bp    DNA        linear    PRI 15-MAR-2002
DEFINITION  Homo sapiens 3p25-26 BAC CTB-187p1 (California Institute of
            Technology BAC Library) complete sequence.
ACCESSION   AC008116
VERSION     AC008116.8  GI:6001959
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 104947)
  AUTHORS   Muzny,D.M., Adams,C., Bailey,M., Barbaria,J., Blankenburg,K.,
            Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,
            Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,
            David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N.,
            Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
            Forcum-Tansey,J., Frantz,P., Ganesh,R., Garcia,D.K., Gorrell,J.H.,
            Gorrell,L.L., Guevara,W., Harris,K., He,X., Hernandez,J.,
            Hodgson,A., Hogues,M., Holloway,C., Hosak,H., Jackson,L.E.,
            Jackson,L., Jia,Y., Jones,M., Kelly,S., Kondejewski,N., Kong,Y.,
            Kovar,C., Leal,B., Li,Z., Lichtarge,O., Liu,J., Liu,W., Logan,O.,
            Lu,J., Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mei,G.,
            Moore,S., Moorish,T., Morgan,M., Morris,S., Nash,S., Nelson,A.,
            Nguyen,R., Nguyen,N., Nguyen,S., Oswal,G., Parish,B., Paxton,S.,
            Payton,B., Perez,L., Pu,L.L., Quiles,M., Reiter,D., Rives,M.,
            Samuel,S., Say,J., Scherer,S., Shah,E., Shen,H., Simon,M.,
            Sparks,A., Stamps,A., Sucgang,R., Tabor,P., Taylor,T., Vasquez,L.,
            Vinson,R., Vo,Q., Wahbah,M., Watlington,S., Weinstock,G.,
            Weinstock,I.R., Williamson,A., Worley,K., Wren,J., Wrensford,G.,
            Yu,W., Zhou,X., Naylor,S.L., Nelson,D. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 104947)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-1999) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3 (bases 1 to 104947)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-SEP-1999) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   4 (bases 1 to 104947)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-OCT-1999) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   5 (bases 1 to 104947)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2000) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   6 (bases 1 to 104947)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Sep 30, 1999 this sequence version replaced gi:5882338.
            INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
            gc-help@bcm.tmc.edu

            CLONE LENGTH: This sequence does not necessarily represent the
            entire insert of this clone. Overlapping regions of clones are only
            sequenced and submitted once, so the sequence for the remainder of
            the insert may be found in the record for the adjacent clones.
            Overlapping clones are noted at the beginning and end of the
            Features listing.

            ANNOTATION OF FEATURES:
            STSs are identified using ePCR (Genome Res. 7:541-550) searches
            of a local database that includes entries from dbSTS, GDB, and
            local mapping efforts.
            Repeats are identified using RepeatMasker (A. Smit and P. Green,
            unpublished.) for Human and Mouse sequences.
            Genes and Region of sequence similarity are identified by BLAST
            (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
            EST and cDNA sequences. Genes demonstrate at least two exons
            flanked by consensus splice sites that maintained sequence
            continuity across the splice junctions. Sequences that are not
            identical matches are annotated as similar.

            SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
            standard of double strand coverage with a minimum of 2 clones and 2
            reads with no ambiguities or 2 chemistries with a minimum of 2
            clones and 3 reads with no ambiguities. If the sequence quality for
            a region does not meet this standard, it will be indicated in the
            annotation as Low Coverage.

            QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
            standards - estimated error rate less than 1 per 10,000 bases.
            Reports of lowest quality individual bases and measures of base
            quality are listed below. Description of the metrics can be found
            at URL:
            http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

            QUALSTAT-REPORT--------

            --------- Summary Statistics ---------
            Contig length:                               104947
            Phrap values in estimate:                    104295
            Average error rate (BCM-Phrap estimate):     0.00014946
            Fraction of Phrap values less than 40 :      0.0217748
            Number of consensus changing edits:          21
            Number of N's in consensus :                 0

            --------- Consensus changing edits ---------
            Position    Original-Context        Edited-Context
            13808       cctgtgtttt(t)ttttattga   cctgtgtttt(t)ttttattga
            14551       gcgagctgag(t)ttacaccctg  gcgagctgag(g)ttacaccctg
            14579       ctgcactcca(n)cctgggcaac  ctgcactcca(g)cctgggcaac
            14610       ttgcctccaa(n)aaaanntat   ttgcctccaa(a)aaaaattat
```
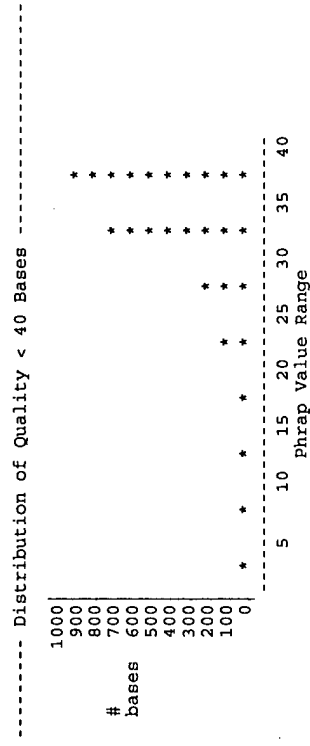
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14613  gcctcaanaa(n)aanntatata    gcctcaaaaa(a)aaattatata
14616  tcaanaanaa(n)ntatatatat    tcaaaaaaaa(a)ttatatatat
14617  caanaanaan(n)tatatatata    caaaaaaaaa(a)tatatatata
15201  tttttttttt(n)ggaganggag    ttttttttt(t)ggagatggag
15207  tttngaga(n)gggtcttac       ttttggaga(t)gggatcttac
15242  tggagtgcag(n)ggcacgatct    tggagtgcag(t)ggcacgatct
22275  gcggtgagcc(n)ccgcgcctgg    gcggtgagcc(a)ccgcgcctgg
22312  aacgtttatg(n)tgattttttt    aacgtttatg(t)tgattttttt
22692  gcccggccag(n)actttaaaa     gcccggccag(a)actttaaaa
23169  tgggaaagg(n)caggccatct     tgggaaagg(g)caggccatct
38915  accgcctcg(n)cctcccaaag     accgcctcg(g)cctcccaaag
39053  tggtggtca(n)ntcctgtaatc    tggtggtcca(c)ttctgtaatc
39054  ggtggctcan(n)tctgtaatcc    ggtggctcac(t)tctgtaatcc
39079  actttggag(n)ccaggcgna      actttggag(g)ccaggcgga
39088  gnccagggcg(n)acagatcact    gccagggcg(g)acagatcact
77261  gaggggaga(n)agagaaagg      gaggggaga(g)agagaaagg
78454  ccgacgggc(n)gtgggtagg      ccgacgggc(c)gtgggtagg
```

---- Distribution of Quality < 40 Bases ----

```
1000 |
 900 |
 800 |
 700 |                                    *
 600 |                                *   *
 500 |                                *   *
 400 |                            *   *   *
 300 |                    *       *   *   *
 200 |                *   *   *   *   *   *
 100 |            *   *   *   *   *   *   *
   0 |    *   *   *   *   *   *   *   *   *
      +---+---+---+---+---+---+---+---+---+
        5  10  15  20  25  30  35  40
              Phrap Value Range
```

```
# 
bases
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FEATURES          Location/Qualifiers
Version: 1.01  xfqo.
source            1..104947
                  /organism="Homo sapiens"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9606"
                  /chromosome="3"
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repeat_region     complement(21..134)
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misc_feature      643..1074
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repeat_region     1938..2343
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repeat_region     complement(4226..4512)
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repeat_region     complement(4908..5023)
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Alignment Scores:
Pred. No.:                              Length:            104947
Score:                  2.07e-40        Matches:           116
Percent Similarity:     99.15%          Conservative:      0
Best Local Similarity:  99.15%          Mismatches:        0
Query Match:            98.30%          Indels:            1
DB:                                     Gaps:              1
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US-10-659-782A-32 (1-116) x AC008116 (1-104947)

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Qy     1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetMetLeuTrpLeuAspLeu 20
Db 47501 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGGTGTTGGCTGGACTTG 47442
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnArgValArgProPro 40
Db 47441 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGAGACCTCCC 47382
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Qy    41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 47381 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCACCAGCTCTGACCTGGAG 47322
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61 GlnGlnArgHis---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
Db 47321 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 47262
         ||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Qy    80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 99
Db 47261 CTCACTGTTTCTGGAAGGACCATGGGGGTTTAGAGTCCTAAACAGACTGTTTCCCCTTCC 47202
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Qy   100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
Db 47201 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 47151
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RESULT 4
AC012515

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                    Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
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                    Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
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                    Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
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                    Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
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                    Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
                    Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
                    Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
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                    Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
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                    Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
                    Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
                    and Gibbs,R.
  TITLE             Direct Submission
  JOURNAL           Unpublished
  REFERENCE         2  (bases 1 to 146947)
  AUTHORS           Worley,K.C.
  TITLE             Direct Submission
  JOURNAL           Submitted (29-OCT-1999) Human Genome Sequencing Center, Department
                    of Molecular and Human Genetics, Baylor College of Medicine, One
                    Baylor Plaza, Houston, TX 77030, USA
  COMMENT           On Jan 7, 2001 this sequence version replaced gi:9929498.
                    -------------- Genome Center
                         Center: Baylor College of Medicine
                         Center code: BCM
                         Web site: http://www.hgsc.bcm.tmc.edu/
                         Contact: hgsc-help@bcm.tmc.edu
                    --------------- Project Information
                         Center project name: HMLC
                         Center clone name: RP11-885J5
                    -------------- Summary Statistics
                         Sequencing vector: M13; L08821
                         Chemistry: Dye-terminator Big Dye: 100% of reads
                         Assembly program: Phrap; version 0.990329
                         Consensus quality: 117566 bases at least Q40
                         Consensus quality: 133456 bases at least Q30
                         Consensus quality: 137976 bases at least Q20
                         Estimated insert size: 138502; sum-of-contigs estimation
                         Estimated insert size: 207623; agarose-fp estimation
                         Quality coverage: 2.4x in Q20 bases; agarose-fp estimation
                         Quality coverage: 3.6x in Q20 bases; sum-of-contigs estimation
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                  * NOTE: Estimated insert size may differ from sequence length
                         (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
                  * NOTE: This is a 'working draft' sequence. It currently
                         consists of 16 contigs. The true order of the pieces
                         is not known and their order in this sequence record is
                         arbitrary. Gaps between the contigs are represented as
                         runs of N, but the exact sizes of the gaps are unknown.
                  * This record will be updated with the finished sequence
                         as soon as it is available and the accesion number will
                         be preserved.
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                  *   43044: contig of 43043 bp in length
                  *   65409: gap of unknown length
                  *   65510: contig of 22366 bp in length
                  *   82660: gap of unknown length
                  *   82661: contig of 17151 bp in length
                  *   82761: gap of unknown length
                  *   96494: contig of 13733 bp in length
                  *   96593: gap of unknown length
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                  *  105307: gap of unknown length
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                  *  105408: contig of 6474 bp in length
                  *  111881: contig of unknown length
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                  *  111981: gap of unknown length
                  *  111982: contig of 8058 bp in length
                  *  120039: gap of unknown length
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                  *  120140: contig of 4680 bp in length
                  *  124819: contig of unknown length
                  *  124919: gap of unknown length
                  *  124920: contig of 5164 bp in length
                  *  130083: gap of unknown length
                  *  130084: gap of unknown length
                  *  130184: contig of 4714 bp in length
                  *  134897: gap of unknown length
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                  *  134998: contig of 3727 bp in length
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ORIGIN

Alignment Scores:
Pred. No.:                                    146947
Score:                       2.9e-40          Matches:              116
Percent Similarity:          605.50           Conservative:         0
Best Local Similarity:       99.15%           Mismatches:           0
Query Match:                 99.15%           Indels:               1
                             98.30%           Gaps:                 1
                             2

US-10-659-782A-32 (1-116) x AC012515 (1-146947)

Qy      1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu  20
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Db  35989 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTTCTCCTCCTCGGCATGCTCTGGCTGGACTTG 36048

Qy     21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnArgValArgProPro  40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  36049 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 36108

Qy     41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  36109 CACAAGGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGTCTCGTGACCTGGAG 36168

Qy     61 GlnGlnArgHis---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp  79
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Db  36169 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCCCAGAGCACAAAGGACTCTGGGTCTGAC 36228

Qy     80 LeuThrValSerGlyArgThrTrpGlyLeuAsnArgLeuPheProProSer  99
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  36229 CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCTAAACAGACTGTTTCCCCCTTCC 36288

Qy    100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
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Db  36289 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 36339

RESULT 5
AC022384/c
LOCUS          AC022384              210053 bp    DNA       linear    PRI 08-NOV-2002
DEFINITION     Homo sapiens chromosome 3 clone RP11-438J1 map 3p, complete
               sequence.
ACCESSION      AC022384
VERSION        AC022384.5   GI:24418051
KEYWORDS       HTG.
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
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REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS   1 (bases 1 to 210053)
             Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
             Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
             Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C.,
             Li,F., Li,G., Li,J., Li,L., Li,L., Liu,T., Liu,Y., Liu,N., Liu,B.,
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             Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X.,
             Wu,B., Wu,Q., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X.,
             Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N.,
             Yu,J. and Yang,H.
TITLE   Chromosome 3p genomic sequence
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 210053)
AUTHORS   Hu,S., Dong,W., Zhang,X., Wang,J., Zhang,Y., Zhang,Y., Liu,B.,
             Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y.,
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             Huang,F., Zhang,G., Li,J., Bian,X., Zhang,X., Zhang,M., Li,L., Feng,X., Yu,J.
             and Yang,H.
TITLE   Direct Submission
JOURNAL   Submitted (03-FEB-2000) Human Genomic Center, Institute of
             Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
             100101, P.R.China
REFERENCE 3 (bases 1 to 210053)
AUTHORS   Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
             Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
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             Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H.,
             Wang,J., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X.,
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             Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B.,
             Zhu,N., Yu,J. and Yang,H.
TITLE   Direct Submission
JOURNAL   Submitted (16-JAN-2001) Human Genomic Center, Institute of
             Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
             100101, P.R.China
REFERENCE 4 (bases 1 to 210053)
AUTHORS   Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
             Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
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             Yu,J. and Yang,H.
TITLE   Direct Submission
JOURNAL   Submitted (29-OCT-2002) Human Genomic Center, Institute of
             Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
             100101, P.R.China
REFERENCE 5 (bases 1 to 210053)
AUTHORS   Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
             Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
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             Yu,J and Yang,H.
TITLE   Direct Submission
JOURNAL   Submitted (08-NOV-2002) Human Genomic Center, Institute of

COMMENT   Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
             100101, P.R.China
             On Oct 29, 2002 this sequence version replaced gi:12232490.
             -----------------Genome Center
             Center:Beijing Center
             Center code:Beijing
             Website:http://hgc.igtp.ac.cn
             http://www.genomics.org.cn
             Contact:hgc@igtp.ac.cn
             -----------------Project Information
             Center project name:1% project
             Center clone name: RP11-438J1
             -----------------Summary Statistics
             Sequencing vector: pUC18; 100% of reads
             Chemistry: Dye-terminator: ET 55% of reads
             Chemistry: Dye-terminator Big Dye; 45% of reads
             Assembly program: Phrap; version 0.990329
             Consensus quality: 212148 bases at least Q40
             Consensus quality: 213483 bases at least Q30
             Consensus quality: 214138 bases at least Q20
             Insert size: 210053; sum-of-contigs
             Quality coverage: 11.98x in Q20 bases;sum-of-contigs
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FEATURES   Location/Qualifiers
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                  /chromosome="3"
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                  /clone="RP11-438J1"

ORIGIN

Alignment Scores:
Pred. No.:   4.14e-40   Length: 210053
Score: 605.50   Matches: 116
Percent Similarity: 99.15%   Conservative: 0
Best Local Similarity: 99.15%   Mismatches: 0
Query Match: 98.30%   Indels: 1
DB: Gaps: 1
                                                             9

US-10-659-782A-32 (1-116) x AC022384 (1-210053)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
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Db 169382 ATGCCCTCCCCAGGGACCGGTCTGCAGCCTGCCTTCCTCGGCATGCTCTGGCTGGACTTG 169323

Qy   21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnArgValArgProPro 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 169322 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGTCCAGGTGAGACCTCC 169263

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 169262 CACAAGGCCCCACATGTGTTCCAGCCCTGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 169203

Qy   61 GlnGlnArgHis--TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
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Db 169202 CAGCAGCGCCATCTCGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCGGGGTCTGAC 169143

Qy   80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 99
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 169142 CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCTTCC 169083

Qy   100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
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Db 169082 AGCAGGAAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCGAGCTC 169032

RESULT 6
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LOCUS   AC012600   216292 bp   DNA   linear   HTG 04-SEP-2000
DEFINITION   Homo sapiens chromosome 3 clone RP1-1082A18, WORKING DRAFT
             SEQUENCE, 11 unordered pieces.
ACCESSION   AC012600

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VERSION     AC012600.10  GI:9966203
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 216292)
  AUTHORS   Muzny,D.M., Adams,C., Bailey,M., Barbaria,J., Blankenburg,K.,
            Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,
            Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen.Z., Cox,C.,
            David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N.,
            Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
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            Tabor,P., Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wahbah,M.,
            Watlington,S., Weinstock,G., Weinstock,I.R., Williamson,A.,
            Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Nelson,D. and
            Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 216292)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-OCT-1999) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Sep 4, 2000 this sequence version replaced gi:919583.
            ---------------------------- Genome Center
            Center: Baylor College of Medicine
            Center code: BCM
            Web site: http://www.hgsc.bcm.tmc.edu/
            Contact: hgsc-help@bcm.tmc.edu
            ---------------------------- Project Information
            Center project name: HMQN
            Center clone name: RP1-1082A18
            ---------------------------- Summary Statistics
            Sequencing vector: M13; L08821
            Chemistry: Dye-terminator Big Dye: 98% of reads
            Assembly program: Phrap; version 0.990329
            Consensus quality: 193458 bases at least Q40
            Consensus quality: 207037 bases at least Q30
            Consensus quality: 210993 bases at least Q20
            Estimated insert size: 213807; sum-of-contigs estimation
            Estimated insert size: 317914; agarose-fp estimation
            Quality coverage: 3x in Q20 bases; agarose-fp estimation
            Quality coverage: 4.4x in Q20 bases; sum-of-contigs estimation
            *  NOTE: Estimated insert size may differ from sequence length
            *  (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            *  NOTE: This is a 'working draft' sequence. It currently
            *  consists of 11 contigs. The true order of the pieces
            *  is not known and their order in this sequence record is
            *  arbitrary. Gaps between the contigs are represented as
            *  runs of N, but the exact sizes of the gaps are unknown.
            *  This record will be updated with the finished sequence
            *  as soon as it is available and the accession number will
            *  be preserved.
            *         1    84660: contig of 84660 bp in length
            *     84661    84760: gap of unknown length
            *     84761   141893: contig of 57133 bp in length
            *    141894   141993: gap of unknown length
            *    141994   157877: contig of 15884 bp in length
            *    157878   157977: gap of unknown length
            *    157978   173768: contig of 15791 bp in length
            *    173769   173868: gap of unknown length
            *    173869   185178: contig of 11310 bp in length
            *    185179   185278: gap of unknown length
            *    185279   192013: contig of 6735 bp in length
            *    192014   192113: gap of unknown length
            *    192114   196844: contig of 4731 bp in length
            *    196845   196944: gap of unknown length
            *    196945   205362: contig of 8418 bp in length
            *    205363   205462: gap of unknown length
            *    205463   210832: contig of 5370 bp in length
            *    210833   210932: gap of unknown length
            *    210933   214884: contig of 3952 bp in length
            *    214885   214984: gap of unknown length
            *    214985   216292: contig of 1308 bp in length.
FEATURES             Location/Qualifiers
     source          1..216292
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="3"
                     /clone="RP1-1082A18"
ORIGIN

Alignment Scores:
Pred. No.:                4.27e-40        Length:          216292
Score:                      605.50        Matches:            116
Percent Similarity:         99.15%        Conservative:         0
Best Local Similarity:      99.15%        Mismatches:           0
Query Match:                98.30%        Indels:               1
DB:                              2        Gaps:                 1

US-10-659-782A-32 (1-116) x AC012600 (1-216292)

Qy      1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 164737 ATGCCCTCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG 164678

Qy     21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 164677 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 164618

Qy     41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 164617 CACAAAGCCCCACATGTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 164558

Qy     61 GlnGlnArgHis--TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
          ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db 164557 CAGCAGCGCCATCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 164498

Qy     80 LeuThrValSerGlyArgThrTrpGlyValLeuAsnArgLeuPheProProSer 99
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 164497 CTCACTGTTTCTGGAAGGACATGGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCTTCC 164438

Qy    100 SerArgGluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db 164437 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGTCGCAGCCCCGAGCTC 164387

RESULT 7
AC090841/c
LOCUS       AC090841              217778 bp    DNA     linear   PRI 08-NOV-2002
DEFINITION  Homo sapiens chromosome 3 clone RP11-1082A18 map 3p, complete
            sequence.
ACCESSION   AC090841
VERSION     AC090841.2  GI:24418046
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 217778)
  AUTHORS   Zhang,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C.,
            Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q.,
            Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N.,
            Li,C., Li,C., Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y.,
```

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Consensus quality: 1239 bases at least Q30
Consensus quality: 1436 bases at least Q20
Insert size: 1445; sum-of-contigs
Quality coverage:   1.32x in Q20 bases;sum-of-contigs
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FEATURES           Location/Qualifiers
source             1..217778
                   /organism="Homo sapiens"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:9606"
                   /chromosome="3"
                   /map="3p"
                   /clone="RP11-1082A18"
ORIGIN

Alignment Scores:
Pred. No.:                              Length:        217778
Score:             605.50               Matches:       116
Percent Similarity: 99.15%              Conservative:  0
Best Local Similarity: 99.15%           Mismatches:    0
Query Match:       98.30%               Indels:        1
DB:                4.3e-40              Gaps:          1

US-10-659-782A-32 (1-116) x AC090841 (1-217778)

Qy      1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8175 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG 8116

Qy     21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8115 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 8056

Qy     41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8055 CACAAAGCCCCACATGTTGTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 7996

Qy     61 GlnGlnArgHis---TrpLeuAspLeuPheSerGlnSerGlyThrLysAspGlySerAsp 79
          |||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db   7995 CAGCAGCGGCATCTCTGGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 7936

Qy     80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 99
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7935 CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCCTAAACACAGACTGTTTCCCCCTTCC 7876

Qy    100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluGlu 116
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7875 AGCAGAGAAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 7825
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RESULT 8
AY372274
LOCUS       AY372274                6008 bp    DNA     linear   PRI 19-APR-2004
DEFINITION  Macaca mulatta ghrelin precursor (GHRL) gene, complete cds.
ACCESSION   AY372274
VERSION     AY372274.1  GI:3541889
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 6008)
  AUTHORS   Angeloni,S.V., Glynn,N., Ambrosini,G., Garant,M.J., Dee Higley,J.,
            Suomi,S. and Hansen,B.C.
  TITLE     Characterization of the rhesus monkey ghrelin gene and factors
            influencing ghrelin gene expression and fasting plasma levels
  JOURNAL   Endocrinology 145 (5), 2197-2205 (2004)
   PUBMED   14736731
REFERENCE   2  (bases 1 to 6008)
  AUTHORS   Angeloni,S.V., Glynn,N.M., Ambrosini,G., Garant,M.J., Higley,J.D.,
            Suomi,S. and Hansen,B.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-AUG-2003) Center for Vaccine Development, University
```

```
TITLE       Liu,N., Liu,B., Liu,Y., Li,L., Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q.,
            Qi,x., Song,L., Song,S., Sun,W., Sun,Y., Tan,X., Tao,R.,
            Wang,H., Wang,J., Wang,J., Wang,J., Wu,D., Xie,F., Xuan,Z., Xue,Y.,
            Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H.,
            Zhang,M., Zhang,X., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhu,B.,
            Zhu,N., Yu,J. and Yang,H.
JOURNAL     Chromosome 3p genomic sequence
REFERENCE   Unpublished
AUTHORS     2 (bases 1 to 217778)
            Zhang,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C.,
            Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q.,
            Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,Y.,
            Li,C., Li,C., Li,F., Li,G., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y.,
            Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y., Luo,C., Luo,J.,
            Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y.,
            Tan,X., Tao,R., Wang,H., Wang,H., Wang,J., Wang,J., Wang,L., Wang,L.,
            Wang,L., Wang,R., Wang,X., Wang,X., Wang,X., Wu,D., Wu,Q., Xie,F.,
            Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
            Zhang,H., Zhang,H., Zhang,Z., Zhang,M., Zhang,X., Zhang,X., Zhang,Y.,
            Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.
TITLE       Direct Submission
JOURNAL     Submitted (11-MAR-2001) Human Genomic Center, Institute of
            Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
            100101, P.R.China
REFERENCE   3 (bases 1 to 217778)
AUTHORS     Zhang,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C.,
            Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q.,
            Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N.,
            Li,C., Li,C., Li,F., Li,G., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y.,
            Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q.,
            Qi,x., Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R.,
            Wang,H., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X.,
            Yang,X., Yu,B., Zeng,Y., Zhang,Y., Zhang,H., Zhang,M., Zhang,N.,
            Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhu,B., Zhu,N., Zhu,N.,
            Yu,J. and Yang,H.
JOURNAL     Direct Submission
            Submitted (29-OCT-2002) Human Genomic Center, Institute of
            Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
            100101, P.R.China
REFERENCE   4 (bases 1 to 217778)
AUTHORS     Zhang,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C.,
            Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q.,
            Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N.,
            Li,C., Li,C., Li,F., Li,G., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y.,
            Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q.,
            Qi,x., Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R.,
            Wang,H., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Yan,C.,
            Zhang,X., Xue,F., Zhang,X., Zhang,G., Zhang,H., Zhang,M., Zhang,N.,
            Yang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhu,B., Zhu,N., Zhu,N.,
            Yu,J. and Yang,H.
JOURNAL     Direct Submission
            Submitted (08-NOV-2002) Human Genomic Center, Institute of
            Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
            10101, P.R.China
COMMENT     On Oct 29, 2002 this sequence version replaced gi:13273353.
            ----------------------Genome Center
            Center:Beijing Center
            Center code:Beijing
            Website:http://hgc.igtp.ac.cn
            http://www.genomics.org.cn
            Contact:hgc@igtp.ac.cn
            ---------------------- Project Information
            Center project name:1% project
            Center clone name: RP11-1082A18
            ----------------------- Summary Statistics
            Sequencing vector: pUC18; 100% of reads
            Chemistry: Dye-terminator: ET 55% of reads
            Chemistry: Dye-terminator Big Dye; 45% of reads
            Assembly program: PhrAp; version 0.990329
            Consensus quality: 956 bases at least Q40
```

```
                    of Maryland, Baltimore, School of Medicine, 685 West Baltimore
                    Street, Baltimore, MD 21201, USA
FEATURES            Location/Qualifiers
  source            1..6008
                    /organism="Macaca mulatta"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9544"
  gene              <1721..>6003
                    /gene="GHRL"
  mRNA              join(<1721..1828,2037..2153,5088..5196,5984..>6003)
                    /gene="GHRL"
                    /product="ghrelin precursor"
  CDS               join(1721..1828,2037..2153,5088..5196,5984..6003)
                    /gene="GHRL"
                    /note="GHS-R1a ligand, hormone; appetite stimulant,
                    stomach secreted"
                    /codon_start=1
                    /product="ghrelin precursor"
                    /protein_id="AAQ74837.1"
                    /db_xref="GI:34541890"
                    /translation="MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRAQQRKESKKP
                    PAKLQPRALGGWLRPEDGDQAEGAEDELEIQFNAPFDVGIKLSGVQYQQHSQALGKFL
                    QDILWEEAKEAPADK"
ORIGIN

Alignment Scores:
Pred. No.:                                Length:            6008
Score:              9.67e-33              Matches:           103
Percent Similarity: 500.50                Conservative:      2
Best Local Similarity: 86.07%             Mismatches:        11
Query Match:        81.25%                Indels:            7
DB:                                       Gaps:              2

US-10-659-782A-32 (1-116) x AY372274 (1-6008)

Qy     1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1721 ATGCCCTCCCCAGGGACCGTCTGTAGCCTCCTGCTCCTCGGCATGCTCTGGCTCGACTTG 1780

Qy    21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnArgValArgProPro 40
         ||||||||||||||||||||||||||||||||||||| ||||||
Db  1781 GCCATGGCAGGCTCCAGCTTCCTGAGCCCCGAACACCAGAGAGCCCAGGTGAGAGCTTCC 1840

Qy    41 HisLysAlaProHisVal------------ValProAlaLeuProLeuSerArgAsnGln 55
         ||||||||||||          |||||||||||||||||||||||
Db  1841 CACAAAGCCCCACATGC-TGACTAGGGTATCTTGTTCCAGCCCCTGGCCACTTGGCAACCAG 1899

Qy    56 LeuCysAspLeuGlnGlnHis---TrpLeuSerValPheSerGlnSerThrLys 74
         ||||||||||||||||||   ||  |||||||||||||||||||
Db  1900 CTCTGTGACCTGGAGCAGCAGCAGTCAATCTCGGGCTTCAGCCCTTCTCCCAGAGACAAAG 1959

Qy    75 AspSerGlySerAspLeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArg 94
         |||||||||||||||| ||:|||||||||  |||||  ||
Db  1960 GACTCTGGGTCTGACCTCACTCTTTCTGGAAGCACATGGGGGCTTGGGGTCCTAAAGAGA 2019

Qy    95 LeuPheProProSerSerArgGluArgSerArgArgSerHisGlnProSerCysSerPro 114
         ||||||||||||||||||||||||||||||||:||||||||||||
Db  2020 CTATTTCCCCTTCCAGCAGCAGAAGAAGGAGTCCAAGAAGCCACCAGAAGCTGCAGCCCCC 2079

Qy   115 GluLeu 116
         ||||||
Db  2080 GAGCTC 2085


RESULT 9
AY455990S1
LOCUS       AY455990S1          362 bp    DNA     linear   MAM 23-MAR-2004
DEFINITION  Cervus elaphus canadensis ghrelin gene, exons 1, 2 and partial cds.
ACCESSION   AY455990
VERSION     AY455990.1  GI:4554386
SEGMENT     1 of 2
SOURCE      Cervus elaphus canadensis (wapiti)
  ORGANISM  Cervus elaphus canadensis
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                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
                    Cervinae; Cervus.
REFERENCE   1 (bases 1 to 362)
  AUTHORS   Dickin,J.C., Thue,T.D. and Buchanan,F.C.
  TITLE     An Investigation into the Mammalian Ghrelin Gene
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 362)
  AUTHORS   Dickin,J.C., Thue,T.D. and Buchanan,F.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-2003) Animal and Poultry Science, University of
            Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada
FEATURES            Location/Qualifiers
  source            1..362
                    /organism="Cervus elaphus canadensis"
                    /mol_type="genomic DNA"
                    /sub_species="canadensis"
                    /db_xref="taxon:9861"
  mRNA              join(<1..91,290..>362)
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  CDS               join(<1..91,290..>362)
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                    /product="ghrelin"
                    /protein_id="AAS67355.1"
                    /db_xref="GI:4545388"
                    /translation="VCSLLLLSVLWLDLAMAGSSFLSPEHQKLQRKEPKKPSGRLKPR
                    ALEGQFDPEV"
  exon              <1..91
                    /number=1
  exon              290..>362
                    /number=2
ORIGIN

Alignment Scores:
Pred. No.:                                Length:            362
Score:              3.42e-10              Matches:           61
Percent Similarity: 220.50                Conservative:      9
Best Local Similarity: 60.87%             Mismatches:        33
Query Match:        53.04%                Indels:            12
DB:                 35.80%                Gaps:              4

US-10-659-782A-32 (1-116) x AY455990S1 (1-362)

Qy     7 ValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeuAlaMetAlaGlySerSer 26
         |||||||||||||||||||||||||||||||||||||||
Db     2 GTCTGCAGCCTGCTCTGCTCCTCAGCGTGCTCTGGCTCGACTTGGCCATGGCGGGGCTCCAGC 61

Qy    27 PheLeuSerProGluHisGlnValArgValGlnArgPro-ProHisLysAlaProHisVa 46
         |||||||||||||||||||:::||||:||||||||    ||||||||||||
Db    62 TTTCTGAGCCCGGAACATCAGAAACTCGAGTGAGCATCACCCCGGAGCCCGCCCCGCAT-- 119

Qy    46 lValProAlaLeuProLeuSerArgAsnGlnLeuCysAspLeuGluGlnGlnArgHisTrpA 66
         ||| |||||||||:|| :::|||   ||
Db   120 ---CCTGAATGCCC------------AAGCCGTGAGCTGGGCAGCAGTCTCTCTGAGC 166

Qy    66 aSerValPheSerGlnSerThrLysAsp---SerGlySerAspLeu---------- 80
         ||| ||||||||||:||| ||:||||
Db   167 TTCAGCTTCTCCCGAGCCAGAAGGAGGGCTCTGATCGTGGGTCCACACCTCA 226

Qy    81 -ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSe 100
         :::          ||||||||:::|| |||:||:
Db   227 CTCTGCTTCTGCAGGGAGGAGGGGGATTCGGGCGCTCAACGGAGCACCTCCTTTTCCTG 286

Qy   100 rArgGluArgSerArgArgSerHisGlnProSerCysSerPro 114
         ||||||:::  ||||||||:  ||||||
Db   287 CAGAGAAAGGAACCTAAGAGCCATCAGGCAGACTGAAGCCCC 329


RESULT 10
AY455987
LOCUS       AY455987          354 bp    DNA     linear   MAM 23-MAR-2004
DEFINITION  Odocoileus virginianus ghrelin gene, exons 1, 2 and partial cds.
ACCESSION   AY455987
VERSION     AY455987.1  GI:4545400
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KEYWORDS   .
SOURCE   Odocoileus virginianus (white-tailed deer)
  ORGANISM   Odocoileus virginianus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
                Odocoileinae; Odocoileus.
REFERENCE   1 (bases 1 to 354)
  AUTHORS   Dickin,J.C., Thue,T.D. and Buchanan,F.C.
  TITLE   An Investigation into the Mammalian Ghrelin Gene
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 354)
  AUTHORS   Dickin,J.C., Thue,T.D. and Buchanan,F.C.
  TITLE   Direct Submission
  JOURNAL   Submitted (02-NOV-2003) Animal and Poultry Science, University of
                Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada
FEATURES   Location/Qualifiers
     source   1..354
                /organism="Odocoileus virginianus"
                /mol_type="genomic DNA"
                /db_xref="taxon:9874"
     mRNA   join(<1..91,290..>354)
                /product="ghrelin"
     CDS   join(<1..91,290..>354)
                /codon_start=2
                /product="ghrelin"
                /protein_id="AAS67361.1"
                /db_xref="GI:45545401"
                /translation="ICSLLLLSVLWLDLAMAGSSFLSPEHQKLQRKEPKKPSGRLKPR
                ALEGQFDP"
     exon   <1..91
                /number=1
     exon   290..>354
                /number=2
ORIGIN

Alignment Scores:
Pred. No.:   1.08e-09   Length: 354
Score: 214.50   Matches: 59
Percent Similarity: 60.87%   Conservative: 11
Best Local Similarity: 51.30%   Mismatches: 33
Query Match: 34.82%   Indels: 12
DB: Gaps: 4

US-10-659-782A-32 (1-116) x AY455987 (1-354)

Qy   7 ValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeuAlaMetAlaGlySer 26
        :||||||||||||||||||||||| :||||||||||||||||||||||||||||
Db   2 ATCTGCAGCCTGCTGCTCCTCAGTGTCCTCTGGCTGGACTTGGCCATGGCAGGGCTCCAGC 61

Qy 27 PheLeuSerProGluHisGlnArgValGlnValArgProProHisLys-AlaProHisVa 46
        ||||||||||||||||:|:|||||:|||| ||| :||||||: |||
Db 62 TTTCTGAGCCCCGAACATCAGAAACTGCAGGTGAGACGTCACCCCAGCACGT-- 119

Qy 46 lValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGluGlnGlnArgHisArgTrpAl 66
        ||| ||| ::: ||| :||
Db 120 ---CCTGAATGCCCC----------AAGCCGTGTGAGCTGGGCAGTGGCTCACCCTGAGC 166

Qy 66 aSerValPheSerGlnSerThrLysAsp--SerGlySerAspLeu---------- 80
        ||||| |||||||||
Db 167 TTCAGCTTTCTCCCCGAGCCCAAAGGACGGGGCTCTGGGTCTGATTGTGGGTCCGCGCTCA 226

Qy 81 -ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSe 100
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Db 227 CTCTGCTTCTCGGAGGAGGGGGGATTCGGGGCCTAAGGGAGGAGCACCTCCTCTTTTCCTG 286

Qy 100 rArgGluArgSerArgArgSerHisGlnProSerCysSerPro 114
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Db 287 CAGAGAAAGGAACCTAAGAAGCCATCAGGCAGACTGAAGCCCC 329

RESULT 11
AR170496
LOCUS   AR170496   351 bp   DNA   linear   PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6291653.

ACCESSION   AR170496
VERSION   AR170496.1   GI:17908455
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 351)
  AUTHORS   Sheppard,P.O. and Deisher,T.A.
  TITLE   Antibodies to motilin homologs
  JOURNAL   Patent: US 6291653-A 1 18-SEP-2001;
FEATURES   Location/Qualifiers
     source 1..351
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Pred. No.:   1.18e-09   Length: 351
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DB: Gaps: 1

US-10-659-782A-32 (1-116) x AR170496 (1-351)

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Qy 21 AlaMetAlaGlySerValPheSerLeuSerProGluHisGlnArgValGlnValArgProPro 40
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Db 61 GCCATGGCAGGGCTCCAGTTCCTGAGCCCTGAACACCAGAGAGTCCAG--------- 108

Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
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Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 108 -------- 108

Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
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Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
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Db 109 CAGAGAAAGGAGTCGAAGAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157

RESULT 12
AR208181
LOCUS   AR208181   351 bp   DNA   linear   PAT 20-JUN-2002
DEFINITION Sequence 1 from patent US 6380158.
ACCESSION   AR208181
VERSION   AR208181.1   GI:21508130
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 351)
  AUTHORS   Sheppard,P.O.
  TITLE   Motilin homologs
  JOURNAL   Patent: US 6380158-A 1 30-APR-2002;
FEATURES   Location/Qualifiers
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Pred. No.:   1.18e-09   Length: 351
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DB:                      6             Gaps:            1

US-10-659-782A-32 (1-116) x AR208181 (1-351)

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Qy   21 AlaMetAlaGlySerPheSerProGluHisValGlnArgValGlnValArgProPro 40
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Db   61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG---------- 108

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerArgAsnGlnLeuCysAspLeuGlu 60
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Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db  108 -------------------------------------------------- 108

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 100
Db  108 -------------------------------------------------- 108

Qy  101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
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Db  109 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157


RESULT 13
AR404108
LOCUS       AR404108          351 bp    DNA    linear    PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6627729.
ACCESSION   AR404108
VERSION     AR404108.1  GI:40152102
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Sheppard,P.O., Deisher,T.A., Jaspers,S.R. and Bishop,P.D.
  TITLE     TML peptides
  JOURNAL   Patent: US 6627729-A 1 30-SEP-2003;
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"

Alignment Scores:
Pred. No.:               1.18e-09      Length:          351
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Best Local Similarity:   43.59%        Mismatches:      0
Query Match:             34.74%        Indels:          65
DB:                      6             Gaps:            1

US-10-659-782A-32 (1-116) x AR404108 (1-351)

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Qy   21 AlaMetAlaGlySerPheSerProGluHisValGlnArgValGlnValArgProPro 40
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Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db  108 -------------------------------------------------- 108

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 100
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Qy  101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
        ::: ||||||||||||||||||||||||||||||||||||||||
Db  109 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157


RESULT 14
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LOCUS       AX062356          351 bp    DNA    linear    PAT 24-JAN-2001
DEFINITION  Sequence 3 from Patent WO0100830.
ACCESSION   AX062356
VERSION     AX062356.1  GI:12540240
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sheppard,P.O., Jaspers,S.R., Deisher,T.A. and Bishop,P.D.
  TITLE     Sgip peptides
  JOURNAL   Patent: WO 0100830-A 3 04-JAN-2001;
            ZymoGenetics, Inc. (US)
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Pred. No.:               1.18e-09      Length:          351
Score:                   214.00        Matches:         51
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Best Local Similarity:   43.59%        Mismatches:      0
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US-10-659-782A-32 (1-116) x AX062356 (1-351)

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Db    1 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG 60

Qy   21 AlaMetAlaGlySerPheSerProGluHisProHisValGlnArgValGlnArgValArgProPro 40
        |||||||||||||||||||||||||||||||||||||||||
Db   61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG---------- 108

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerArgAsnGlnLeuCysAspLeuGlu 60
Db  108 -------------------------------------------------- 108

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db  108 -------------------------------------------------- 108

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 100
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Db      108 ---------------------------------------------------------- 108

Qy      101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
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Db      109 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157


RESULT 15
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LOCUS       AX154581              351 bp    DNA        linear    PAT 22-JUN-2001
DEFINITION  Sequence 1 from Patent WO0138355.
ACCESSION   AX154581
VERSION     AX154581.1  GI:14536167
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sheppard,P.O., Jaspers,S.R., Deisher,T.A. and Bishop,P.D.
  TITLE     Method of forming a peptide-receptor complex with zsig33 and
            therapeutic use thereof
  JOURNAL   Patent: WO 0138355-A 1 31-MAY-2001;
            ZymoGenetics, Inc. (US)
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ORIGIN
Alignment Scores:
Pred. No.:                   1.18e-09        Length:         351
Score:                       214.00          Matches:        51
Percent Similarity:          44.44%          Conservative:   1
Best Local Similarity:       43.59%          Mismatches:     1
Query Match:                 34.74%          Indels:         65
DB:                          6               Gaps:           1

US-10-659-782A-32 (1-116) x AX154581 (1-351)

Qy        1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
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Db      108 ---------------------------------------------------------- 108

Qy       61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80

Db      108 ---------------------------------------------------------- 108

Qy       81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100

Db      108 ---------------------------------------------------------- 108

Qy      101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
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Db      109 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157
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GenCore version 5.1.6
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DT 07-NOV-2001 (first entry)
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DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36846.
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KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
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OS Homo sapiens.
XX
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PF 17-JAN-2001; 2001WO-US001354.
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PR 04-FEB-2000; 2000US-0180628P.
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XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Barash SC, Ruben SM;
XX
DR   WPI; 2001-483426/52.
XX
PT   Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS   Disclosure; SEQ ID NO 36846; 3071pp + Sequence Listing; English.
XX
CC   AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC   amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC   activity, and can be used in gene therapy and vaccine production. (I)
CC   proteins and polynucleotides may be used in the prevention, diagnosis and
CC   treatment of diseases associated with inappropriate (I) expression. For
CC   example, they may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
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CC    that affect the activity of (I) by expressing inactive proteins or to
CC    supplement the patients own production of (I). Additionally, (I)
CC    polynucleotides may be used to produce the secreted (I), by inserting the
CC    nucleic acids into a host cell and culturing the cell to express the
CC    protein. (I) proteins and polynucleotides may be used to prevent,
CC    diagnose and treat immune/haematopoietic-related diseases, especially
CC    cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC    to AAK87694 represent human immune/haematopoietic antigen genomic
CC    sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC    represent sequences used in the exemplification of the present invention
XX
SQ    Sequence 5034 BP; 1049 A; 1324 C; 1291 G; 1370 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                3.33e-53        Length:            5034
Score:                    605.50          Matches:           116
Percent Similarity:       99.15%          Conservative:      0
Best Local Similarity:    99.15%          Mismatches:        0
Query Match:              98.30%          Indels:            1
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US-10-659-782A-32 (1-116) x AAK82034 (1-5034)

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Qy     21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnArgValArgProPro  40
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Qy     41 HisLysAlaProHisValValProAlaLeuProLeuSerArgAsnGlnLeuCysAspLeuGlu  60
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Db   4914 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG  4855

Qy     61 GlnGlnArgHis---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp  79
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Db   4854 CAGCAGCGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC  4795

Qy     80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer  99
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Db   4794 CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC  4735

Qy    100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu  116
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Db   4734 AGCAGAGAAAGGAGTCGAAGAAGCCACCACGCCAAGCTGCAGCCCCGAGCTC  4684
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AC    ABA16829;
XX
DT    23-JAN-2002 (first entry)
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DE    Human nervous system related polynucleotide SEQ ID NO 9160.
XX
KW    Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW    immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW    antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW    antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW    antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW    antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW    neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS    Homo sapiens.
XX
PN    WO200159063-A2.
XX
PD    16-AUG-2001.
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PF    17-JAN-2001; 2001WO-US001334.
XX
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XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Barash SC, Ruben SM;
XX
DR   WPI; 2001-541565/60.
XX
PT   Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating nervous system cancers
PT   and metastases.

XX
PS   Disclosure; SEQ ID NO 9160; 1701pp + Sequence Listing; English.
XX
CC   The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC   (ABB14678-ABB18001) useful for preventing, treating or ameliorating
CC   medical conditions e.g. by protein or gene therapy. The genes are
CC   isolated from a range of human tissues disclosed in the specification.
CC   The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC   the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC   ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC   breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC   disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC   anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC   multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC   cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC   ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC   infectious diseases such as viral, bacterial, fungal and parasitic
CC   infections. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 5034 BP; 1049 A; 1324 C; 1291 G; 1370 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   Length: 5034
Score: 3.33e-53   Matches: 116
Percent Similarity: 605.50   Conservative: 0
Best Local Similarity: 99.15%   Mismatches: 0
Query Match: 99.15%   Indels: 1
                      98.30%   Gaps: 1
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US-10-659-782A-32 (1-116) x ABA16829 (1-5034)

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Db   5034 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG 4975

Qy   21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4974 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 4915

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
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Qy   61 GlnGlnArgHis---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
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Qy   80 LeuThrValSerGlyArgThrTrpGlyLeuValLeuAsnArgLeuPheProProSer 99
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4794 CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 4735

Qy   100 SerArgGluArgArgSerHisGlnProSerCysSerProGluLeu 116
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Db   4734 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 4684

RESULT 3
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XX
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XX
DT   07-NOV-2001 (first entry)
XX
DE   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36845.
XX
KW   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW   cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200157182-A2.

us-10-659-782a-32.rng

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XX
PD   09-AUG-2001.
XX
PF   17-JAN-2001;   2001WO-US001354.
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XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,   Barash SC,   Ruben SM;
XX
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DR   WPI; 2001-483426/52.
XX
PT   Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS   Disclosure; SEQ ID NO 36845; 3071pp + Sequence Listing; English.
XX
CC   AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC   amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC   activity, and can be used in gene therapy and vaccine production. (I)
CC   proteins and polynucleotides may be used in the prevention, diagnosis and
CC   treatment of diseases associated with inappropriate (I) expression. For
CC   example, they may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of (I) by expressing inactive proteins or to
CC   supplement the patients own production of (I). Additionally, (I)
CC   polynucleotides may be used to produce the secreted (I), by inserting the
CC   nucleic acids into a host cell and culturing the cell to express the
CC   protein. (I) proteins and polynucleotides may be used to prevent,
CC   diagnose and treat immune/haematopoietic-related diseases, especially
CC   cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC   to AAK87694 represent human immune/haematopoietic antigen genomic
CC   sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 5036 BP; 1049 A; 1323 C; 1293 G; 1371 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   3.33e-53   Length: 5036
Score: 605.50   Matches: 116
Percent Similarity: 99.15%   Conservative: 0
Best Local Similarity: 99.15%   Mismatches: 0
Query Match: 98.30%   Indels: 1
DB: 4   Gaps: 1

US-10-659-782A-32 (1-116) x AAK82033 (1-5036)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5036 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCCTCGGCATGCTCTGGCTGGACTTG 4977

Qy   21 AlaMetAlaGlySerProPheLeuSerProGluHisGlnArgValGlnArgValArgProPro 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4976 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 4917

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4916 CACAAAGCCCACATGTTGTTCCAGCCCTGCCCATTAGCAACCAGCTCTGTGACCTGGAG 4857

Qy   61 GlnGlnArgHis---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   4856 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 4797

Qy   80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 99
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4796 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGCTGTTCCCCCTTCC 4737

Qy   100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluGlu 116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4736 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 4686

RESULT 4
AAK82030/c
ID   AAK82030 standard; DNA; 5036 BP.
XX
AC   AAK82030;
XX
DT   -07-NOV-2001 (first entry)
XX
DE   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36842.
XX
KW   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW   cytostatic; gene therapy; vaccine; metastasis; ds.

```
PA  (HUMA-) HUMAN GENOME SCI INC.
XX
PI  Rosen CA, Barash SC, Ruben SM;
XX
DR  WPI; 2001-483426/52.
XX
PT  Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT  useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS  Disclosure; SEQ ID NO 36842; 3071pp + Sequence Listing; English.
XX
CC  AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC  amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC  activity, and can be used in gene therapy and vaccine production. (I)
CC  proteins and polynucleotides may be used in the prevention, diagnosis and
CC  treatment of diseases associated with inappropriate (I) expression. For
CC  example, they may be used to treat disorders associated with decreased
CC  expression by rectifying mutations or deletions in a patient's genome
CC  that affect the activity of (I) by expressing inactive proteins or to
CC  supplement the patients own production of (I). Additionally, (I)
CC  polynucleotides may be used to produce the secreted (I), by inserting the
CC  nucleic acids into a host cell and culturing the cell to express the
CC  protein. (I) proteins and polynucleotides may be used to prevent,
CC  diagnose and treat immune/haematopoietic-related diseases, especially
CC  cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC  to AAK87694 represent human immune/haematopoietic antigen genomic
CC  sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC  represent sequences used in the exemplification of the present invention
XX
SQ  Sequence 5036 BP; 1050 A; 1324 C; 1293 G; 1369 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                           Length:           5036
Score:                 3.33e-53      Matches:           116
Percent Similarity:      99.15%      Conservative:        0
Best Local Similarity:   99.15%      Mismatches:          0
Query Match:             98.30%      Indels:              1
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US-10-659-782A-32 (1-116) x AAK82030 (1-5036)

Qy     1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
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Db  5036 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG 4977

Qy    21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4976 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 4917

Qy    41 HisLysAlaProHisValProAlaLeuProLeuSerArgAsnGlnLeuCysAspLeuGlu 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4916 CACAAAGCCCCACATGTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 4857

Qy    61 GlnGlnArgHis--TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
           |||||||||      |||||||||||||||||||||||||||||||||||||||||
Db  4856 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 4797

Qy    80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 99
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4796 CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCTAAACAGACTGTTTCCCCCTTCC 4737

Qy   100 SerArgGluArgSerHisGlnProSerCysSerProGluLeu 116
           ||||||||||||||||||||||||||||||||||||||||||
Db  4736 AGCAGAGAAAGGAGTCGAAGAGAGCCCAGCCAAGCTGCAGCCCCCAGCTC 4686

RESULT 5
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ID  ABA16827 standard; DNA; 5036 BP.
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AC  ABA16827;
XX
DT  23-JAN-2002 (first entry)
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DE   Human nervous system related polynucleotide SEQ ID NO 9158.
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KW   Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW   immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW   antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW   antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW   antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW   antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS   Homo sapiens.
XX
PN   WO200159063-A2.
XX
PD   16-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001334.
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PR   11-DEC-2000; 2000US-0254097P.
PR   05-JAN-2001; 2001US-0259678P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Barash SC, Ruben SM;
XX
DR   WPI; 2001-541565/60.
XX
PT   Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating nervous system cancers
PT   and metastases.
XX
PS   Disclosure; SEQ ID NO 9158; 1701pp + Sequence Listing; English.
XX
CC   The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC   (ABB14678-ABB18001) useful for preventing, treating or ameliorating
CC   medical conditions e.g. by protein or gene therapy. The genes are
CC   isolated from a range of human tissues disclosed in the specification.
CC   The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC   the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC   ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC   breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC   disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC   anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC   multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC   cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC   ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC   infectious diseases such as viral, bacterial, fungal and parasitic
CC   infections. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 5036 BP; 1050 A; 1324 C; 1293 G; 1369 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   3.33e-53   Length: 5036
Score: 605.50   Matches: 116
Percent Similarity: 99.15%   Conservative: 0
Best Local Similarity: 99.15%   Mismatches: 0
Query Match: 98.30%   Indels: 1
DB: 5   Gaps: 1

US-10-659-782A-32 (1-116) x ABA16827 (1-5036)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu   20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5036 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCGGCATGCTCTGGCTGGACTTG 4977

Qy   21 AlaMetAlaGlySerPheLeuSerProGluHisGlnValGlnValArgProPro   40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4976 GCCATGGCAGGCTCCAGCTTCTCAGCCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 4917

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerArgAsnGlnLeuCysAspLeuGlu   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4916 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTGAGCCTCTGTGACCTGGAG 4857

Qy   61 GlnGlnArgHis---TrpAlaSerValPheSerGlnThrLysAspSerThrGlySerGlySerAsp   79
           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   4856 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 4797

Qy   80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer   99
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4796 CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCTTCC 4737

Qy   100 SerArgGluArgArgSerHisGlnProSerCysSerProGluLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||

Db   4736 AGCAGAGAAAGAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 4686

RESULT 6
ABA16828/c
ID   ABA16828 standard; DNA; 5036 BP.
XX
AC   ABA16828;
XX
DT   23-JAN-2002 (first entry)
XX
DE   Human nervous system related polynucleotide SEQ ID NO 9159.
XX
KW   Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW   immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW   antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW   antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW   antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW   antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS   Homo sapiens.
XX
PN   WO200159063-A2.
XX
PD   16-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001334.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
PR   14-AUG-2000; 2000US-0224518P.
PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225213P.
PR   14-AUG-2000; 2000US-0225214P.
PR   14-AUG-2000; 2000US-0225266P.
PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
PR   14-AUG-2000; 2000US-0225270P.
PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
PR   14-AUG-2000; 2000US-0225759P.
PR   18-AUG-2000; 2000US-0226279P.
PR   22-AUG-2000; 2000US-0226681P.
PR   22-AUG-2000; 2000US-0226868P.
PR   22-AUG-2000; 2000US-0227182P.
PR   23-AUG-2000; 2000US-0227009P.
PR   30-AUG-2000; 2000US-0228924P.
PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   05-SEP-2000; 2000US-0229513P.
PR   06-SEP-2000; 2000US-0230437P.
PR   06-SEP-2000; 2000US-0230438P.
PR   08-SEP-2000; 2000US-0231242P.

PR   08-SEP-2000;   2000US-0231243P.
PR   08-SEP-2000;   2000US-0231244P.
PR   08-SEP-2000;   2000US-0231413P.
PR   08-SEP-2000;   2000US-0231414P.
PR   08-SEP-2000;   2000US-0232080P.
PR   08-SEP-2000;   2000US-0232081P.
PR   12-SEP-2000;   2000US-0231968P.
PR   14-SEP-2000;   2000US-0232397P.
PR   14-SEP-2000;   2000US-0232398P.
PR   14-SEP-2000;   2000US-0232399P.
PR   14-SEP-2000;   2000US-0232400P.
PR   14-SEP-2000;   2000US-0232401P.
PR   14-SEP-2000;   2000US-0233063P.
PR   14-SEP-2000;   2000US-0233064P.
PR   14-SEP-2000;   2000US-0233065P.
PR   21-SEP-2000;   2000US-0234223P.
PR   21-SEP-2000;   2000US-0234274P.
PR   25-SEP-2000;   2000US-0249997P.
PR   25-SEP-2000;   2000US-0249998P.
PR   26-SEP-2000;   2000US-0235484P.
PR   27-SEP-2000;   2000US-0235834P.
PR   27-SEP-2000;   2000US-0258836P.
PR   29-SEP-2000;   2000US-0236327P.
PR   29-SEP-2000;   2000US-0236367P.
PR   29-SEP-2000;   2000US-0236368P.
PR   29-SEP-2000;   2000US-0236369P.
PR   29-SEP-2000;   2000US-0236370P.
PR   02-OCT-2000;   2000US-0236802P.
PR   02-OCT-2000;   2000US-0237037P.
PR   02-OCT-2000;   2000US-0237038P.
PR   02-OCT-2000;   2000US-0237039P.
PR   02-OCT-2000;   2000US-0237040P.
PR   13-OCT-2000;   2000US-0239935P.
PR   13-OCT-2000;   2000US-0239937P.
PR   20-OCT-2000;   2000US-0409960P.
PR   20-OCT-2000;   2000US-0241785P.
PR   20-OCT-2000;   2000US-0241786P.
PR   20-OCT-2000;   2000US-0241787P.
PR   20-OCT-2000;   2000US-0241808P.
PR   20-OCT-2000;   2000US-0241809P.
PR   20-OCT-2000;   2000US-0241826P.
PR   20-OCT-2000;   2000US-0242221P.
PR   01-NOV-2000;   2000US-0246617P.
PR   08-NOV-2000;   2000US-0246474P.
PR   08-NOV-2000;   2000US-0246475P.
PR   08-NOV-2000;   2000US-0246476P.
PR   08-NOV-2000;   2000US-0246477P.
PR   08-NOV-2000;   2000US-0246478P.
PR   08-NOV-2000;   2000US-0246523P.
PR   08-NOV-2000;   2000US-0246524P.
PR   08-NOV-2000;   2000US-0246525P.
PR   08-NOV-2000;   2000US-0246526P.
PR   08-NOV-2000;   2000US-0246527P.
PR   08-NOV-2000;   2000US-0246528P.
PR   08-NOV-2000;   2000US-0246532P.
PR   08-NOV-2000;   2000US-0246609P.
PR   08-NOV-2000;   2000US-0246610P.
PR   08-NOV-2000;   2000US-0246611P.
PR   08-NOV-2000;   2000US-0246613P.
PR   17-NOV-2000;   2000US-0249207P.
PR   17-NOV-2000;   2000US-0249208P.
PR   17-NOV-2000;   2000US-0249209P.
PR   17-NOV-2000;   2000US-0249210P.
PR   17-NOV-2000;   2000US-0249211P.
PR   17-NOV-2000;   2000US-0249212P.
PR   17-NOV-2000;   2000US-0249213P.
PR   17-NOV-2000;   2000US-0249214P.
PR   17-NOV-2000;   2000US-0249215P.
PR   17-NOV-2000;   2000US-0249216P.
PR   17-NOV-2000;   2000US-0249217P.
PR   17-NOV-2000;   2000US-0249218P.
PR   17-NOV-2000;   2000US-0249244P.
PR   17-NOV-2000;   2000US-0249245P.

PR   17-NOV-2000;   2000US-0249264P.
PR   17-NOV-2000;   2000US-0249265P.
PR   17-NOV-2000;   2000US-0249297P.
PR   17-NOV-2000;   2000US-0249299P.
PR   17-NOV-2000;   2000US-0249300P.
PR   01-DEC-2000;   2000US-0250391P.
PR   01-DEC-2000;   2000US-0251160P.
PR   05-DEC-2000;   2000US-0251030P.
PR   05-DEC-2000;   2000US-0251988P.
PR   05-DEC-2000;   2000US-0256719P.
PR   06-DEC-2000;   2000US-0251479P.
PR   08-DEC-2000;   2000US-0251856P.
PR   08-DEC-2000;   2000US-0251868P.
PR   08-DEC-2000;   2000US-0251869P.
PR   08-DEC-2000;   2000US-0251989P.
PR   08-DEC-2000;   2000US-0251990P.
PR   11-DEC-2000;   2000US-0254097P.
PR   05-JAN-2001;   2001US-0259678P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,   Barash SC,   Ruben SM;
XX
DR   WPI; 2001-541565/60.
XX
PT   Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating nervous system cancers
PT   and metastases.
XX
PS   Disclosure; SEQ ID NO 9159; 1701pp + Sequence Listing; English.
XX
CC   The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC   (ABB14678-ABB18001) useful for preventing, treating or ameliorating
CC   medical conditions e.g. by protein or gene therapy. The genes are
CC   isolated from a range of human tissues disclosed in the specification.
CC   The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC   the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC   ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC   breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC   disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC   anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC   multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC   cardiovascular disorders e.g 01 myocardial ischaemias; (d) wound healing
CC   ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC   infectious diseases such as viral, bacterial, fungal and parasitic
CC   infections. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 5036 BP; 1049 A; 1323 C; 1371 T; 1293 G; 0 U; 0 Other;
XX

Alignment Scores:
Pred. No.:   5036
Score: 3.33e-53
                       605.50   Matches: 116
Percent Similarity: 99.15%   Conservative: 0
Best Local Similarity: 99.15%   Mismatches: 0
Query Match: 98.30%   Indels: 1
DB: 5   Gaps: 1

US-10-659-782A-32 (1-116) x ABA16828 (1-5036)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5036 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGACTTG 4977

Qy   21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnArgValArgProPro 40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4976 GCCATGGCAGGCTCCAGCTTCCTCAGCCCTGAACACCAGAGAGTGAGACCTCCC 4917

Qy   41 HisLysAlaProHisValValProLeuSerAsnGlnLeuCysAspLeuGlu 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4916 CACAAAGCCCACATGTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 4857

CC   animal and assaying for the presence of a genotype in the animal which is
CC   associated with favourable growth, appetite and fatness, the genotype
CC   characterised by a polymorphism in the ghrelin gene. The composition and
CC   methods are useful in screening animals (i.e. pigs) to determine those
CC   more or less likely to produce desired growth, appetite and fatness to
CC   optimise breeding and selection techniques. The present sequence is
CC   porcine ghrelin consensus DNA spanning exon 1 and exon 2 of the
CC   invention.
XX
SQ   Sequence 447 BP; 93 A; 133 C; 140 G; 81 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   447
Score: 5.9e-14   Matches: 65
Percent Similarity: 57.81%   Conservative: 9
Best Local Similarity: 50.78%   Mismatches: 36
Query Match: 35.71%   Indels: 18
DB: 12   Gaps: 5

US-10-659-782A-32 (1-116) x ADK66746 (1-447)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeu---Asp 19
         |||||||| || ||||||||| :::|||||||||||| ::: |||
Db   11 ATGCCCTCCACGGGACCATTTGCAGCCTGCTGCTCCTCAGCGTGCTCCATGGCAGAC 70

Qy   20 LeuAlaMetAlaGlySerPheLeuSerProGluHisGlnHisValGlnValArgPro 39
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   71 TTGGCCATGGCAGGGCTCCAGCTTCTTGAGCCCGAACACCAGAAAGTGCAGTAAGACGT 130

Qy   40 ProHisLysAlaPro-------HisValValProAlaLeuProLeuSerArgAsnGln 55
         ::|||||||||| :::||:::||||||||||||||||
Db 131 CTCCCAGAGCCCGGCCCTTGGCGGGTACCTCATCCCAGCCTTCATGAGTTGGGACC 190

Qy   56 LeuCysAspLeuGlnGlnArgHisTrpAlaSerValPheSerGlnSer--ThrLysA 75
         ||||||| ||||||||
Db 191 TGGGCTCACCTG-----------CTCTGGGCTTCAGGCCTCTCCCAGGAGGACTCTGG 238

Qy   75 Sp--SerGlySerAspLeuThrVal------------------SerGlyArgThrTrpG 88
         || ||||||
Db 239 ATCTGCAAGGAGGCCCATACCTTGCTCGTTCTGGAAGGAAGTAGTGGGGTGGGTGGG 298

Qy   88 lyLeuArgValLeuAsnArgLeuPheProProSerArgGluArgSerArgArgSerH 108
         || ||| |||||| ||
Db 299 CATCTTAGGGCTTCAAGAGAGCAGTTCCTCTTTCCAGCAGCAGAAAGGAGTCCAAGAAGCC 358

Qy 108 isGlnProSerCysSerPro 114
         |||||::: |||||||
Db 359 AGCAGCCAAACTGAAGCCCC 378

RESULT 8
AAX04550
ID   AAX04550 standard; cDNA; 351 BP.
XX
AC   AAX04550;
XX
DT   07-APR-1999 (first entry)
XX
DE   cDNA encoding a protein designated zsig33.
XX
KW   Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
KW   nutrient absorption regulation; obesity; metabolic disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..351
FT   /tag= a
FT   /note= "no termination codon"
FT   sig_peptide   1..69
FT   /tag= b
FT   mat_peptide   70..351
FT   /tag= c
XX

Qy   61 GlnGlnArgHis---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
         ||||||||| ||||||||||||||||||||||||||||||||||||
Db 4856 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCCCCAGAGCACAAAGGACTCTGGGTCTGAC 4797

Qy   80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 99
         ||||||||||||||||||||||||||||||||||||||||||||
Db 4796 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTTCTAAACAGACTGTTTCCCCTTCC 4737

Qy 100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
         ||||||||||||||||||||||||||||||||||||||
Db 4736 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 4686

RESULT 7
ADK66746
ID   ADK66746 standard; DNA; 447 BP.
XX
AC   ADK66746;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Porcine ghrelin consensus DNA spanning exon 1 and exon 2.
XX
KW   Growth; appetite; fatness; genotype; polymorphism; ghrelin protein;
KW   breeding; porcine; ds.
XX
OS   Sus sp.
XX
FH   Key   Location/Qualifiers
FT   misc_feature   1..121
FT   /tag= a
FT   /note= "Ghrelin protein"
FT   misc_signal   11..13
FT   /tag= b
FT   /note= "Initiation codon"
FT   variation   replace(145,A)
FT   /tag= c
FT   /standard_name= "Single nucleotide polymorphism (SNP)"
FT   variation   replace(250,G)
FT   /tag= d
FT   /standard_name= "Single nucleotide polymorphism (SNP)"
FT   misc_feature   336..447
FT   /tag= e
FT   /note= "Ghrelin protein"
FT   variation   replace(440,T)
FT   /tag= f
FT   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   US2003211512-A1.
XX
PD   13-NOV-2003.
XX
PF   14-NOV-2002; 2002US-00294191.
PR   14-NOV-2001; 2001US-0333222P.
XX
PA   (ROTH/) ROTHSCHILD M F.
PA   (KIMK/) KIM K.
PA   (ANDE/) ANDERSON L L.
XX
PI   Rothschild MF, Kim K, Anderson LL;
XX
DR   WPI; 2004-010667/01.
XX
PT   Screening animals (i.e. pigs) to determine those more likely to produce
PT   desired growth, appetite and fatness to optimize breeding and selection
PT   techniques comprises detecting the presence of a polymorphism in the
PT   Ghrelin gene.
XX
PS   Disclosure; SEQ ID NO 11; 24pp; English.
XX
CC   The present invention relates to a method of screening animals to
CC   determine those more likely to produce desired growth, appetite and
CC   fatness which involves obtaining a sample of genetic material from the

PN   WO9842840-A1.
XX
PD   01-OCT-1998.
XX
PF   23-MAR-1998;   98WO-US005620.
XX
PR   24-MAR-1997;   97US-0041102P.
PR   24-MAR-1997;   97US-00822897.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Sheppard PO, Deisher TA;
XX
DR   WPI; 1999-070071/06.
DR   P-PSDB; AAW87991.
XX
PT   Human polypeptide having homology to motilin, zsig33 - useful e.g. to
PT   treat gastrointestinal motility disorders, obesity etc. and to identify
PT   antagonists to treat gastrointestinal hypermotility.
XX
PS   Claim 5; Page 54-55; 69pp; English.
XX
CC   The present sequence encodes a protein designated Zsig33. The nucleic
CC   acids are strongly expressed in stomach tissue. The polypeptide (or
CC   allelic variants/orthologs) can be used to stimulate gastric motility,
CC   measured as increased transit time or gastric emptying of an ingested
CC   substance in mammals. The products are used to treat disorders associated
CC   with gastrointestinal cell contractility, secretion of digestive
CC   enzymes/acids, gastrointestinal motility, recruitment of digestive
CC   enzymes, gastrointestinal inflammation, reflux disease and nutrient
CC   absorption regulation. Zsig33 polypeptides may also be important in
CC   neurologically, since the family of gut-brain peptides to which the
CC   homologous protein motilin belongs has been associated with neurological
CC   and CNS functions. They may therefore be used e.g. to regulate satiety or
CC   treat obesity and other metabolic disorders where neurological feedback
CC   modulates nutritional absorption. They are useful to identify zsig33
CC   agonists, antagonists and ligands and to produce antibodies
XX
SQ   Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   Length: 351
Score: 1.84e-13   Matches: 51
Percent Similarity: 44.44%   Conservative: 1
Best Local Similarity: 43.59%   Mismatches: 0
Query Match: 34.74%   Indels: 65
DB: 2   Gaps: 1

US-10-659-782A-32 (1-116) x AAX04550 (1-351)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTCGACTTG 60

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG------------ 108

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 108 -- 108

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 108 -- 108

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db 108 -- 108

Qy 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
          ::: ||||| || ||||||||||||||||||||||||||||
Db 109 CAGAGAAAGGAGTCGAAGAGCCACCAGCCAAGCTGCAGCCCCCCGAGCTC 157

RESULT 9
AAF30033
ID   AAF30033 standard; DNA; 351 BP.
XX
AC   AAF30033;
XX
DT   23-APR-2001 (first entry)
XX
DE   DNA encoding zsig33.
XX
KW   SGIP; zsig33; human; chromosome 3p26.1; anorectic; antidiabetic;
KW   nutritional absorption modulator; growth hormone secretagogue;
KW   somatotropin; somatomedin-C; gene therapy; SB.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   sig_peptide   1..69
FT   /*tag=   a
FT   mat_peptide   70..351
FT   /*tag=   b
XX
PN   WO200100830-A1.
XX
PD   04-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US018306.
XX
PR   30-JUN-1999; 99US-00345157.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
DR   WPI; 2001-123010/13.
DR   P-PSDB; AAB20101.
XX
PT   Novel variants of SGIP peptides for modulating contractility in duodenum
PT   or jejunum tissue, pancreatic pancreatic secretion of hormones and digestive
PT   enzymes, inducing growth hormone secretion or modulating gastric
PT   emptying.
XX
PS   Disclosure; 54; 61pp; English.
XX
CC   The present sequence is that of DNA encoding zsig33 (see AAB20101), a
CC   secreted protein with homology to motilin (see AAB20102). Human zsig33 is
CC   expressed at high levels in the stomach, and at lower levels in the small
CC   intestine and pancreas. A novel peptide fragment of zsig33, termed SGIP
CC   (see AAB20100), is claimed. SGIP is a ligand for growth hormone
CC   secretagogue receptor, and is therefore useful for modulating secretion
CC   of growth hormone and insulin like growth factor 1. SGIP, and variant
CC   SGIP peptides, are used in claimed methods for stimulating
CC   contractability in duodenum or jejunum tissue, modulating pancreatic
CC   secretion of hormones and digestive enzymes, inducing growth hormone
CC   secretion, and modulating gastric emptying
XX
SQ   Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   Length: 351
Score: 1.84e-13   Matches: 51
Percent Similarity: 44.44%   Conservative: 1
Best Local Similarity: 43.59%   Mismatches: 0
Query Match: 34.74%   Indels: 65
DB: 4   Gaps: 1

US-10-659-782A-32 (1-116) x AAF30033 (1-351)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTCGACTTG 60

CC   pancreatic enzymes and hormones, secretion of insulin-like growth factor
CC   -I, secretion of non-zsig33 proteins. It is useful for modulating growth
CC   hormone secretion in a mammal having a disease associated with abnormal
CC   levels of growth hormone, such as osteoporosis, bone repair, bone
CC   remodeling, low osteoblast levels, cartilage repair and remodeling,
CC   skeletal dysplasia, immune suppression, obesity, growth retardation,
CC   protein catabolic responses after surgery, cachexia, protein loss,
CC   dwarfism, wound healing and ovulation induction, treating a mammal having
CC   a metabolic disorder requiring neurological feedback, such as satiety
CC   regulation, glucose absorption and metabolism and neuropathy-associated
CC   gastrointestinal disorders, and stimulating glucose-induced insulin
CC   release in a mammal. The present sequence represents the cDNA encoding
CC   the human zsig33 polypeptide, a peptide ligand for the G-protein coupled
CC   receptor, GHS-R;
XX
SQ   Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   1.84e-13   Length: 351
Score: 214.00   Matches: 51
Percent Similarity: 44.44%   Conservative: 1
Best Local Similarity: 43.59%   Mismatches: 0
Query Match: 34.74%   Indels: 65
DB: 4   Gaps: 1

US-10-659-782A-32 (1-116) x AAF83678 (1-351)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCGGCATGCTCTGGCTGGACTTG 60

Qy   21 AlaMetAlaGlySerPheLeuSerProGluHisValValProPro 40
          ||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGTCCAG----------- 108

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeu 60
Db   108 ----------- 108

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db   108 ----------- 108

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db   108 ----------- 108

Qy 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
          ::: ||||||||||||||||||||||||||||||||||
Db 109 CAGAGAAAGGAGTCGAAGAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157

RESULT 11
ABV72214
ID ABV72214 standard; DNA; 351 BP.
XX
AC ABV72214;
XX
DT 05-DEC-2002 (first entry)
XX
DE Nucleotide sequence of a human zsig33.
XX
KW Short gastrointestinal peptide; SGIP; zsig33; motilin; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..351
FT   /tag= a
FT   /product= "zsig33"
FT   /note= "no termination codon given"
FT sig_peptide   1..69
FT   /tag= b
FT mat_peptide   70..3510

Qy   21 AlaMetAlaGlySerPheLeuSerProGluHisValValProAlaLeuProLeuSerGlnValArgProPro 40
          |||||||||||||||||||||||||||||||||||||||||
Db   61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGTCCAG----------- 108

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeu 60
Db   108 ----------- 108

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db   108 ----------- 108

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db   108 ----------- 108

Qy 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
          ::: ||||||||||||||||||||||||||||||||||
Db 109 CAGAGAAAGGAGTCGAAGAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157

RESULT 10
AAF83678
ID AAF83678 standard; cDNA; 351 BP.
XX
AC AAF83678;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human zsig33 polypeptide encoding cDNA.
XX
KW zsig33; signal transduction; hormone; enzyme; neural development;
KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
KW glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R;
KW G-protein coupled receptor; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..351
FT   /tag= a
FT   /product= "zsig33"
FT   /note= "the stop codon is not indicated"
XX
PN WO200138355-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US032074.
XX
PR 22-NOV-1999; 99US-0166765P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
DR WPI; 2001-355879/37.
DR P-PSDB; AAB62649.
XX
PT Forming reversible peptide receptor complex for purifying cell and
PT peptides, stimulating signal transduction and modulating hormone
PT secretion, involves contacting a receptor with zsig33 polypeptide.
XX
PS Example 2; Page 93-94; 111pp; English.
XX
CC The invention relates to a method of forming a reversible peptide-
CC receptor complex that involves providing an immobilized receptor, and
CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
CC is useful for purifying cells, purifying a peptide, stimulating signal
CC transduction in a cell expressing a receptor. It is also useful for
CC modulating secretion of hormones, neural development and/or utilization,
CC gastric contractility, nutrient uptake, secretion of digestive and

```
FT                /*tag= c
XX
PN   US6420521-B1.
XX
PD   16-JUL-2002.
XX
PF   30-JUN-2000;  2000US-00608810.
XX
PR   30-JUN-1999;  99US-0141592P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
DR   WPI; 2002-634794/68.
DR   P-PSDB; ABB78319.
XX
PT   New Short Gastrointestinal Peptide, which has homology to motilin, useful
PT   for preventing, diagnosing and treating gastrointestinal disorders.
XX
PS   Disclosure; Col 37-40; 23pp; English.
XX
CC   The present sequence encodes human zsig33. The specification describes a
CC   short gastrointestinal peptide (SGIP), which is derived from zsig33. SGIP
CC   has homology to motilin. The SGIP peptide may be used in the prevention,
CC   diagnosis and treatment of diseases associated with inappropriate SGIP
CC   expression. For example, SGIP may be used to treat disorders associated
CC   with decreased expression by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of SGIP by expressing inactive
CC   proteins or to supplement the patients own production of SGIP. SGIP may
CC   also be used as an antigen in the production of antibodies against SGIP
CC   and in assays to identify modulators of SGIP expression and activity. The
CC   anti-SGIP antibodies, agonists and antagonists may also be used to
CC   regulate expression and activity. The anti-SGIP antibody may also be
CC   used as diagnostic agents for detecting the presence of SGIP in samples
XX
SQ   Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:            1.84e-13        Length:             351
Score:               214.00          Matches:             51
Percent Similarity:   44.44%         Conservative:         1
Best Local Similarity: 43.59%        Mismatches:           0
Query Match:          34.74%         Indels:              65
DB:                                   Gaps:                1

US-10-659-782A-32 (1-116) x ABV72214 (1-351)
```

```
Qy    1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTCCTGCTCGGCATGCTGTCTGGACTTG 60

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisArgValGlnValArgProPro 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG---------- 108

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
          --------------------------------------------------------- 108

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerValPheSerGlnSerThrLysAspSerAspLeu 80
          --------------------------------------------------------- 108

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
          --------------------------------------------------------- 108

Qy  101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
          :::  |||||||||||||||||||||||||||||||||||||
Db  109 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157

RESULT 12
```

```
ADI33327
ID   ADI33327 standard; cDNA; 351 BP.
XX
AC   ADI33327;
XX
DT   22-APR-2004 (first entry)
XX
DE   Motilin homologous Zsig33 protein encoding DNA.
XX
KW   motilin; secretin gastric inhibitory peptide; SGIP; contractility;
KW   duodenum; jejunum; pancreatic secretion; hormone; digestive enzyme;
KW   growth hormone secretion; gastric emptying; gene; ss; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..351
FT                   /*tag=  a
XX
PN   US2003176640-A1.
XX
PD   18-SEP-2003.
XX
PF   01-JUL-2002;  2002US-00186414.
XX
PR   30-JUN-1999;  99US-0141592P.
PR   30-JUN-2000;  2000US-00608810.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
DR   WPI; 2003-898590/82.
DR   P-PSDB; ADI33328.
XX
PT   New secretin gastic inhibitory peptides (SGIP), useful for modulating
PT   contractility in duodenum or jejunum tissue, the pancreatic secretion of
PT   hormones and digestive enzymes, or gastric emptying, inducing growth
PT   hormone secretion.
XX
PS   Disclosure; SEQ ID NO 3; 26pp; English.
XX
CC   The invention relates to novel polynucleotides, polypeptides, peptides,
CC   variants and used thereof for peptide fragments which have homology to
CC   motilin. The invention further provides agonists, variants, antibodies,
CC   and host cells expressing the cDNA encoding the novel secretin gastric
CC   inhibitory peptide (SGIP). The invention further relates to: modulating
CC   contractility in duodenum or jejunum tissue by administering the isolated
CC   polypeptide to the tissue; modulating the pancreatic secretion of
CC   hormones and digestive enzymes by administering the isolated polypeptide
CC   to the mammal; inducing growth hormone secretion by administering the
CC   polypeptide to the mammal; modulating gastric emptying by administering
CC   the isolated polypeptide to the mammal. The polypeptide and methods are
CC   useful for modulating contractility in duodenum or jejunum tissue,
CC   modulating the pancreatic secretion of hormones and digestive enzymes,
CC   inducing growth hormone secretion, and modulating gastric emptying. This
CC   polynucleotide sequence represents the DNA encoding a motilin homologous
CC   Zsig33 protein of the invention.
XX
SQ   Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:            1.84e-13        Length:             351
Score:               214.00          Matches:             51
Percent Similarity:   44.44%         Conservative:         1
Best Local Similarity: 43.59%        Mismatches:           0
Query Match:          34.74%         Indels:              65
DB:                                   Gaps:                1

US-10-659-782A-32 (1-116) x ADI33327 (1-351)

Qy    1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    1 ATGCCCTCCCCAGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisValGlnArgValGlnValArgProPro  40

Db   61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG-----------  108
        ||||||||||||||||||||||||||||||||||||||||||||||||
Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerArgAsnGlnLeuCysAspLeuGlu  60

Db  108 ------                                                         108

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu   80

Db  108 ------                                                         108

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer  100

Db  108 ------                                                         108

Qy  101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu            116
        :::  ||||||||||||||||||||||||||||||||||||||||||||||||
Db  109 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCCAAGCTGCAGCCCCGAGCTC            157
```

RESULT 13
ADN11752
ID   ADN11752 standard; cDNA; 351 BP.
XX
AC   ADN11752;
XX
DT   15-JUL-2004   (first entry)
XX
DE   Human zsig33 coding sequence.
XX
KW   ss; gene; human; zsig33; body weight; body mass; antibody; antagonist;
KW   gastrointestinal; antiinflammatory; antiulcer; vulnerary;
KW   growth hormone secretagogue; GHS-R; peptide-antibody complex.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..351
FT   /tag= a
FT   /product= "zsig33"
FT   /partial
FT   /note= "no stop codon"
XX
PN   WO200403645-A2.
XX
PD   22-APR-2004.
XX
PF   06-OCT-2003; 2003WO-US031804.
XX
PR   07-OCT-2002; 2002US-0416918P.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Jaspers SR, Sheppard PO, Bishop PD, Kuijper JL, Deisher TA;
XX
DR   WPI; 2004-340913/31.
DR   P-PSDB; ADN11753.
XX
PT   Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,
PT   inhibiting signal transduction in a cell expressing a growth hormone
PT   secretagogue receptor, or treating a metabolic disorder.
XX
PS   Example 2; Page 88; 100pp; English.
XX
CC   The present invention relates to the use of a zsig33 peptide for forming
CC   a peptide-antibody complex, purifying a peptide, inhibiting signal
CC   transduction in a cell expressing a growth hormone secretagogue receptor
CC   (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite
CC   of a mammal, inhibiting growth hormone secretion in pituitary cells of a
CC   mammal, or treating a metabolic disorder. The peptide is useful for
CC   forming a peptide-antibody complex, purifying a peptide, inhibiting
CC   signal transduction in a cell expressing a GHS-R, decreasing fat
CC   deposition in a mammal, suppressing the appetite of a mammal, inhibiting
CC   growth hormone secretion in pituitary cells of a mammal, or treating a
CC   metabolic disorder. The zsig33 polypeptides can be used to study
CC   proliferation or differentiation in stomach, lung, pituitary,
CC   hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine,
CC   skeletal muscle or pancreas. They are also useful in delivering
CC   therapeutic agents. Zsig33 polypeptides, agonists and antagonists are
CC   also useful for promoting wound healing. The polypeptides, nucleic acids
CC   and antibodies are useful for diagnosing, treating or preventing
CC   disorders associated with gastric reflux, gastroparesis, modulation of
CC   secretion of pituitary hormones, including growth hormone, Crohn's
CC   disease, metabolic wasting, gastric ulcers, weight management, or
CC   degenerative disease. The present sequence is the human zsig33 coding
CC   sequence.
XX
SQ   Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   Length: 351
Score: 1.84e-13   Matches: 51
Percent Similarity: 44.00%   Conservative: 1
Best Local Similarity: 44.44%   Mismatches: 0
Query Match.:   43.59%   Indels: 65
DB: 34.74%   Gaps: 1
                       12

US-10-659-782A-32 (1-116) x ADN11752 (1-351)

```
Qy    1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu   20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGCCCTCCCCAGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG   60

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisValGlnArgValGlnValArgProPro  40
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG-----------  108

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerArgAsnGlnLeuCysAspLeuGlu  60

Db  108 ------                                                         108

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu   80

Db  108 ------                                                         108

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer  100

Db  108 ------                                                         108

Qy  101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu            116
        :::  ||||||||||||||||||||||||||||||||||||||||||||||||
Db  109 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCCAAGCTGCAGCCCCGAGCTC            157
```

RESULT 14
AAD50726
ID   AAD50726 standard; DNA; 401 BP.
XX
AC   AAD50726;
XX
DT   02-APR-2003   (first entry)
XX
DE   Human exon 3-deleted ghrelin DNA.
XX
KW   Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
KW   breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
KW   cancer; human; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   33..308
FT   /tag= a
FT   /product= "Human exon 3-deleted ghrelin protein"
XX

PN   WO200290387-A1.
XX
PD   14-NOV-2002.
XX
PF   10-MAY-2002; 2002WO-AU000582.
XX
PR   10-MAY-2001; 2001AU-00004919.
PR   17-DEC-2001; 2001AU-00009567.
XX
PA   (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
XX
PI   Chopin LK, Jeffery PL, Herington AC;
XX
DR   WPI; 2003-111957/10.
DR   P-PSDB; AAE33410.
XX
PT   Identifying a cancer cell or tissue for treating prostate, ovarian,
PT   breast cancer, or benign prostatic hyperplasia, by detecting the
PT   expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
PT   1b proteins or nucleic acids.
XX
PS   Example 1; Fig 1; 50pp; English.
XX
CC   The invention relates to a method for identifying a cancer cell or tissue
CC   of the reproductive system by detecting expression of a ghrelin, an exon-
CC   3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic acids. The
CC   antibodies, exon 3-deleted form of the preproghrelin and antagonists are
CC   useful for treating cancer of the reproductive system such as prostate,
CC   ovarian, breast, cervical or uterine cancer, choriocarcinoma or benign
CC   prostatic hyperplasia. The present sequence is human exon 3-deleted
CC   ghrelin DNA
XX
SQ   Sequence 401 BP; 92 A; 129 C; 108 G; 72 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   2.2e-13   Length: 401
Score: 214.00   Matches: 51
Percent Similarity: 44.44%   Conservative: 1
Best Local Similarity: 43.59%   Mismatches: 0
Query Match: 34.74%   Indels: 65
DB: Gaps: 8

US-10-659-782A-32 (1-116) x AAD50726 (1-401)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   33 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG 92

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnArgProPro 40
            |||||||||||||||||||||||||||||||||||||||||||||
Db   93 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG----------- 140

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60

Db   140 -- 140

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80

Db   140 -- 140

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100

Db   140 -- 140

Qy   101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
            ::: |||||||||||||||||||||||||||||||||||
Db   141 CAGAGAAACGGAGTCGAAGAAGCCACCAGCAAGCTGCAGCCCCCCAGCTC 189

RESULT 15
AAF59645
ID   AAF59645 standard; cDNA; 494 BP.
XX
AC   AAF59645;

XX
DT   24-APR-2001 (first entry)
XX
DE   Human ghrelin preproprotein cDNA, SEQ ID NO:7.
XX
KW   Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
KW   calcium concentration elevation; infant growth disorder;
KW   growth hormone deficiency; ss.
XX
OS   Homo sapiens.
XX
PN   WO200107475-A1.
XX
PD   01-FEB-2001.
XX
PF   24-JUL-2000; 2000WO-JP004907.
XX
PR   23-JUL-1999;   99JP-00210002.
PR   29-NOV-1999;   99JP-00338841.
PR   26-APR-2000; 2000JP-00126623.
XX
PA   (KANG/) KANGAWA K.
XX
PI   Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
XX
DR   WPI; 2001-159704/16.
DR   P-PSDB; AAB60511.
XX
PT   New peptide compounds which induce growth hormone secretion and elevate
PT   cell calcium concentrations, useful in treatment and diagnosis of infant
PT   growth disorders.
XX
PS   Claim 42; Page 183-184; 210pp; Japanese.
XX
CC   The invention relates to a novel peptide compound or its salt which
CC   induces the secretion of growth hormone and/or elevates calcium ion
CC   concentration in cells. The peptides are ghrelin homologues and are
CC   characterised in that at least one amino acid has been substituted by a
CC   modified amino acid and/or a non-amino acid compound. The invention also
CC   encompasses the unmodified peptides; the DNA encoding the peptides;
CC   vectors and host cells comprising such DNA; a method of producing the
CC   peptides comprising recombinant production, optionally followed by
CC   chemical modification; an antibody specific for a peptide of the
CC   invention; and an assay and kit for detecting the peptides. The peptides
CC   of the invention are useful for treating and/or diagnosing diseases
CC   caused by a deficiency in growth hormone expression or activity. In
CC   particular, they are useful for promoting infant growth due to growth
CC   hormone deficiency. The compounds of the invention are safe with no
CC   accompanying side effects. The present sequence represents cDNA encoding
CC   a ghrelin-type growth hormone secretagogue (GHS) precursor protein of the
CC   invention
XX
SQ   Sequence 494 BP; 111 A; 156 C; 138 G; 89 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   2.89e-13   Length: 494
Score: 214.00   Matches: 51
Percent Similarity: 44.44%   Conservative: 1
Best Local Similarity: 43.59%   Mismatches: 0
Query Match: 34.74%   Indels: 65
DB: Gaps: 1

US-10-659-782A-32 (1-116) x AAF59645 (1-494)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   34 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG 93

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnArgProPro 40
            |||||||||||||||||||||||||||||||||||||||||||||
Db   94 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG---------- 141

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60

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Qy     61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu  80

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Qy     81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer  100

Db    141 ----------------------------------------  141

Qy    101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu  116
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Db    142 CAGAGAAAGGAGTCGAAGAGACCACCAGCCAAGCTGCAGCCCCGAGCTC  190
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Search completed: February 10, 2005, 14:22:08
Job time : 417 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 10, 2005, 13:49:58 ; Search time 85 Seconds
(without alignments)
970.018 Million cell updates/sec

Title: US-10-659-782A-32
Perfect score: 616
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                Fgapop 6.0 , Fgapext 7.0
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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued Patents_NA:*
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                6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Match Length	DB	ID	Description
	1	214	34.7	351	3	US-09-046-479-1	Sequence 1, Appli
	2	214	34.7	351	3	US-08-822-897C-1	Sequence 1, Appli
	3	214	34.7	351	4	US-09-608-810A-3	Sequence 3, Appli
	4	214	34.7	351	4	US-09-404-417A-1	Sequence 1, Appli
	5	214	34.7	654	4	US-10-140-002-441	Sequence 441, App
	6	91.5	14.9	9377	4	US-09-801-874-3	Sequence 3, Appli
c	7	87	14.1	969	4	US-09-252-991A-12776	Sequence 12776, A
c	8	87	14.1	2266	4	US-09-213-767-1	Sequence 1, Appli
c	9	85	13.8	536165	4	US-09-214-808-1	Sequence 1, Appli
c	10	82.5	13.4	867	4	US-09-252-991A-13395	Sequence 13395, A
c	11	82.5	13.4	2103	4	US-09-252-991A-13604	Sequence 13604, A
c	12	82.5	13.4	3222	4	US-09-252-991A-13746	Sequence 13746, A
	13	81.5	13.2	5267	3	US-08-976-255-2	Sequence 2, Appli
	14	81	13.1	8285	4	US-09-732-025-3	Sequence 3, Appli
	15	81	13.1	11827	3	US-09-739-455-3	Sequence 3, Appli
	16	80.5	13.1	111282	3	US-09-754-250-3	Sequence 3, Appli
c	17	79.5	12.9	539	4	US-09-270-767-1719	Sequence 1719, Ap
c	18	79.5	12.9	539	4	US-09-270-767-17001	Sequence 17001, A
	19	79.5	12.9	2135	4	US-07-938-333A-3	Sequence 3, Appli
	20	79.5	12.9	2135	1	US-08-660-216A-3	Sequence 3, Appli
	21	79.5	12.9	5816	3	US-08-857-076-11	Sequence 11, Appl
	22	78.5	12.8	652	3	US-08-998-416-962	Sequence 962, App
c	23	78.5	12.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	24	78.5	12.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	25	78	12.7	1500	4	US-09-489-039A-2848	Sequence 2848, Ap
	26	78	12.7	1518	4	US-09-489-039A-2774	Sequence 2774, Ap
c	27	77.5	12.6	856	4	US-09-535-008-55	Sequence 55, Appl
	28	77.5	12.6	34094	4	US-09-292-034-1	Sequence 1, Appli
c	29	77	12.5	864	4	US-09-252-991A-2337	Sequence 2337, Ap
	30	77	12.5	2088	4	US-09-252-991A-2576	Sequence 2576, Ap
c	31	76.5	12.4	1020	4	US-09-252-991A-3809	Sequence 3809, Ap
	32	76.5	12.4	1122	4	US-09-252-991A-3853	Sequence 3853, Ap
	33	76.5	12.4	1197	4	US-10-037-616-8	Sequence 8, Appli
c	34	76	12.3	1504	2	US-08-839-008-4	Sequence 4, Appli
	35	76	12.3	1506	2	US-08-839-008-6	Sequence 6, Appli
	36	76	12.3	2374	4	US-09-347-801-3	Sequence 3, Appli
	37	76	12.3	2374	4	US-09-854-731-3	Sequence 3, Appli
	38	75.5	12.3	2790	4	US-08-985-950-21	Sequence 21, Appl
	39	75.5	12.3	2790	4	US-09-546-049-21	Sequence 21, Appl
	40	75.5	12.3	2922	4	US-09-310-463-1	Sequence 1, Appli
	41	75.5	12.3	2922	4	US-08-842-248A-1	Sequence 1, Appli
	42	75.5	12.3	4748	4	US-08-426-630-29	Sequence 29, Appl
	43	75	12.2	850	4	US-09-895-652A-6	Sequence 6, Appli
	44	75	12.2	4286	3	US-09-413-304-7	Sequence 7, Appli
	45	75	12.2	4286	4	US-09-817-856-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-046-479-1
; Sequence 1, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
;   APPLICANT: Sheppard, Paul O.
;   APPLICANT: Deisher, Theresa A.
;   TITLE OF INVENTION: MOTILIN HOMOLOGS
;   NUMBER OF SEQUENCES: 7
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: ZymoGenetics, Inc.
;   STREET: 1201 Eastlake Avenue East
;   CITY: Seattle
;   STATE: WA
;   COUNTRY: USA
;   ZIP: 98102
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/046,479
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Sawislak, Deborah A
;   REGISTRATION NUMBER: 37,438
;   REFERENCE/DOCKET NUMBER: 97-04
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 206-442-6672
;   TELEFAX: 206-442-6678
;   TELEX:

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;   SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/822,897C
;     FILING DATE:
;     CLASSIFICATION:  536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Sawislak, Deborah A
;     REGISTRATION NUMBER:  37,438
;     REFERENCE/DOCKET NUMBER:  97-04
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  206-442-6672
;     TELEFAX:   206-442-6678
;     TELEX:
; INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  351 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  Coding Sequence
;     LOCATION:  1..351
;   OTHER INFORMATION:
;     NAME/KEY:  sig_peptide
;     LOCATION:  1..69
;   OTHER INFORMATION:
;     NAME/KEY:  mat_peptide
;     LOCATION:  70..351
;   OTHER INFORMATION:
US-08-822-897C-1

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Score:                   5.14e-17        Matches:            51
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Best Local Similarity:   43.59%          Mismatches:          0
Query Match:             34.74%          Indels:             65
DB:                                      Gaps:                1

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Qy   21 AlaMetAlaGlySerPheLeuSerProGluHisValGlnArgValGlnValArgProPro 40
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Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60

Db  108 -------

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80

Db  108 -------

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100

Db  108 -------

Qy  101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
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RESULT 3
US-09-608-810A-3
; Sequence 3, Application US/09608810A
; Patent No. 6420521
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;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  Coding Sequence
;     LOCATION:  1..351
;   OTHER INFORMATION:
;     NAME/KEY:  sig_peptide
;     LOCATION:  1..69
;   OTHER INFORMATION:
;     NAME/KEY:  mat_peptide
;     LOCATION:  70..351
;   OTHER INFORMATION:
US-09-046-479-1

Alignment Scores:
Pred. No.:                               Length:            351
Score:                   5.14e-17        Matches:            51
Percent Similarity:      44.44%          Conservative:        1
Best Local Similarity:   43.59%          Mismatches:          0
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US-10-659-782A-32 (1-116) x US-09-046-479-1 (1-351)

Qy    1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
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Db    1 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG 60

Qy   21 AlaMetAlaGlySerPheLeuSerProGluHisValGlnArgValGlnValArgProPro 40
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Db   61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG--------- 108

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60

Db  108 -------

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80

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Db  108 -------

Qy  101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
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Db  109 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCCAGCTC 157

RESULT 2
US-08-822-897C-1
; Sequence 1, Application US/08822897C
; Patent No. 6380158
; GENERAL INFORMATION:
;   APPLICANT:  Sheppard, Paul O.
;   APPLICANT:  Deisher, Theresa A.
;   TITLE OF INVENTION:  MOTILIN HOMOLOGS
;   NUMBER OF SEQUENCES:  7
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  ZymoGenetics, Inc.
;     STREET:  1201 Eastlake Avenue East
;     CITY:  Seattle
;     STATE:  WA
;     COUNTRY:  USA
;     ZIP:  98102
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  DOS
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; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608,810A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(351)
; NAME/KEY: sig_peptide
; LOCATION: (1)...(69)
; NAME/KEY: mat_peptide
; LOCATION: (70)...(351)
US-09-608-810A-3

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Score: 5.14e-17   Length: 351
Percent Similarity: 214.00   Matches: 51
Best Local Similarity: 44.44%   Conservative: 1
Query Match: 43.59%   Mismatches: 0
DB: 34.74%   Indels: 65
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US-10-659-782A-32 (1-116) x US-09-608-810A-3 (1-351)

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Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
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Qy 81 ThrValSerGlyArgThrTrpLeuArgValLeuAsnArgLeuPheProSerProGluLeu 116
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Db 108 --- 108

Qy 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
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Db 109 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157

RESULT 4
US-09-404-417A-1
; Sequence 1, Application US/09404417A
; Patent No. 627729
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: TML PEPTIDES
; FILE REFERENCE: 97-04C1
; CURRENT APPLICATION NUMBER: US/09/404,417A
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(351)
US-09-404-417A-1

Alignment Scores:
Pred. No.:
Score: 5.14e-17   Length: 351
Percent Similarity: 214.00   Matches: 51
Best Local Similarity: 44.44%   Conservative: 1
Query Match: 43.59%   Mismatches: 0
DB: 34.74%   Indels: 65
                             4   Gaps: 1

US-10-659-782A-32 (1-116) x US-09-404-417A-1 (1-351)

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Qy 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgArgProPro 40
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Db 61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG---------- 108

Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 108 --- 108

Qy 61 GlnGlnArgHisTrpLeuArgValLeuAsnArgLeuPheProSerProGluLeu 116
Db 108 --- 108

Qy 81 ThrValSerGlyArgThrTrpLeuArgValLeuAsnArgLeuPheProSerProSer 100
Db 108 --- 108

Qy 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
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Db 109 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157

RESULT 5
US-10-140-002-441
; Sequence 441, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550

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; SEQ ID NO 441
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-002-441

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Pred. No.:              1.3e-16      Length:         654
Score:                  214.00       Matches:        51
Percent Similarity:     44.44%       Conservative:   1
Best Local Similarity:  43.59%       Mismatches:     0
Query Match:            34.74%       Indels:         65
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US-10-659-782A-32 (1-116) x US-10-140-002-441 (1-654)

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Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisValProAlaLeuArgProPro 40
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Db  236 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG--------- 283

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Db  283 ------- 283

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db  283 ------- 283

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db  283 ------- 283

Qy  101 Arg-GluArgSerArgArgSerHisGlnProSerProGluLeu 116
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Db  284 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 332


RESULT 6
US-09-801-874-3
; Sequence 3, Application US/09801874
; Patent No. 6582935
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN AMINOTRANSFERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: AMINOTRANSFERASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000615
; CURRENT APPLICATION NUMBER: US/09/801,874
; CURRENT FILING DATE: 8001-03-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9377
; TYPE: DNA
; ORGANISM: Human
US-09-801-874-3

Alignment Scores:
Pred. No.:              4.3          Length:         9377
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Percent Similarity:     39.47%       Conservative:   10
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Qy   21 AlaMetAlaGlySer---SerPheLeuSerProGluHisGlnValGlnValArgPro 39
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Db 4579 AAAATGGCAGACAAGCCAAGCTATTTATGTCCTTTCCTGTTAATGTCCCACCTTCAGCC 4638
Qy   40 ProHisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeu 59
         ::::||||||
Db 4639 AGTGACTCCAGCCCACACT------CCAGTACCTCTGTCCCGCTCCTCTGT--TTC 4689
Qy   60 GluGlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
         |||    |||||||    :::|||
Db 4690 CCATGTACCAGCTAGTGGGGGGCTGTGTTCCCACAGAACTGCATGGACTCG------ 4740
Qy   80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeu-PheProProSe 99
         |||        :::|||    |||:::
Db 4741 ------TCTTCCAGGACATGGCGTTTACAGTTTATGAATACTCTGTCTGGGACCCCA 4791
Qy   99 rSerArgGluArgSerArgArgSerHisGlnProSerCys 112
         |||    |||
Db 4792 AGAAGCTATGCATGGACCCCGA---CATACTCCTCAATGT 4828


RESULT 7
US-09-252-991A-12776/c
; Sequence 12776, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12776
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12776

Alignment Scores:
Pred. No.:              0.515        Length:         969
Score:                  87.00        Matches:        42
Percent Similarity:     38.00%       Conservative:   15
Best Local Similarity:  28.00%       Mismatches:     51
Query Match:            14.12%       Indels:         43
DB:                                  Gaps:           5

US-10-659-782A-32 (1-116) x US-09-252-991A-12776 (1-969)

Qy    2 ProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeuAla 21
         |||    |||    :::|||:::||||||||
Db  507 CCAGACGTAGGTGAGTGATGTCCCACCACACCTGATTGGGATGCTCGGTCCGAATTCGCG 448
Qy   22 MetAlaGlySerSerPheLeuSerPro 30
         :::
Db  447 GTTCAGCCGATTCGGATATTCCGGCGCTCAACCATGGCCGTGTTTGTAGGCGTGCGAGCC 388
Qy   31 ------GluHisGlnArgValGlnValArgProHisLys 42
         |||    :::
Db  387 CGGTTGCTTGCTGACCAGGCCCAGCTCACGCATCCAACCTACGCACTCGGAAACGGCCGAT 328
Qy   43 ------AlaProHisValProAlaLeu-----Pro 51
         |||    |||
Db  327 GGTCACGCCCCTCTTCGCGCAGCATGCCACGGATGCTGCGCGTCGCCGCCGCGCCCCGACT 268
Qy   52 LeuSerAsnGlnLeuCysAspLeuGluGlnGlnArgHisTrpAlaSerValPheSerGln 71
         :::||||||    ||||:::|||
Db  267 CTGGCTGAACAACTGGTTGACCTGGCCTACGGCGCCACGGCCGCCATCGA-CACGCC 209
```

Qy   72 SerThrLysAspSerGlySerAspLeuThrValSerGlyArgThrTrpGlyLeuArgVal 91
              ::: |||| ||| |||||||
Db   208 GCCGTCGAAGAGCGGTGGACGT----------AGTAGCAAGACCGCGCCACTTCGAAAG 161

Qy   92 LeuAsnArgLeuPhePro Pro-----------------SerSerArgGluArg 103
              |||||||||| ||:::||
Db   160 CTGAACAGACCACTTCCACCGACTCCGTCTCACTGGTCTATCAGCGCGTACGATC 101

Qy   104 SerArgArgSerHisGlnProSerCysSer 113
              |||||| |||||||||
Db   100 GAGTTCGTCGACATCAAGAGAGCTGTAGC 71

RESULT 8
US-09-213-767-1
; Sequence 1, Application US/09213767
; Patent No. 5948680
; GENERAL INFORMATION:
;   APPLICANT: Brenda F. Baker
;   APPLICANT: Lex M. Cowsert
;   TITLE OF INVENTION: ANTISENSE MODULATION OF ELK-1 EXPRESSION
;   FILE REFERENCE: RTS-0024
;   CURRENT APPLICATION NUMBER: US/09/213,767
;   CURRENT FILING DATE: 1998-12-17
;   NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
;   LENGTH: 2266
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (316)..(1602)
US-09-213-767-1

Alignment Scores:
Pred. No.:   1.82
Score: 87.00
Percent Similarity: 35.86%   Length: 2266
Best Local Similarity: 28.28%   Matches: 41
Query Match: 14.12%   Conservative: 11
                                                       Mismatches: 47
                                                       Indels: 46
                                                       Gaps: 8

US-10-659-782A-32 (1-116) x US-09-213-767-1 (1-2266)

Qy   2 ProSerProGlyThrValCysSerLeu----------LeuLeuLeuGlyMetLeuTrpLeu 18
              |||||||| :::|||| :::|||| |||||::::|||
Db   797 CCTTCACCATCCAGTCTGCAGCCGCGCACCCCTCATCCTGGCCGTGCTGTGG---- 853

Qy   19 AspLeuAlaMetAlaGlySerSerPheLeuSerPro--GluHisGlnArgValGlnVal 37
              ||||| ::: |||||
Db   854   TGCTCCCCAATGCAGCTCCTGCAGGGGCAGCAG 886

Qy   38 ArgProProHisAlaProHisValVal-----------ProAlaLeuProLeu 52
              |||||| ||:|||
Db   887 CGCCCCCCTCGGGGAGCAGGAGCACCAGTCCAAGCCCTTGTCTCGGAGGCTG 946

Qy   53 SerAsnGlnLeuCys---------------------------------- 57
              ||:|||
Db   947 AAGAGGCGCGGCTTGCCTCGTCAGTCATCCTGACCCGCCGAGGCCCCAAACCTGAAAT 1006

Qy   58 -----AspLeuGluGlnHisArgHisTrpAlaSerValPheSerGlnSerThrLysAsp 75
                   ||| ||| ||| ::: |||
Db 1007 CGGAAGAGCTTAATGTGGAGCCGGGTTTGGGCCGGCTTGCCCCAGAAGTGAAAGTAG 1066

Qy   76 SerGlySerAspLeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeu 95
              |||||| ::::::
Db 1067 AAGGGC-----------CCAAGGAAGAGTTGGAAGTTGCCGGGGAGGAGGGGTTTG 1111

Qy   96 PhePro-----------ProSerSerArgGluArgSerHisGlnProSer 111
              ||||| ::|::||
Db 1112 TGCCAGAAACCACCAAGGCCGAGCCAGAGTCCCTCCACAGGAGGCGTGCCAGCCCCGC 1171

Qy   112 CysSerProGluLeu 116

Db 1172 TGC--CCGCGGTTG 1183
              ||| ||| |||

RESULT 9
US-09-214-808-1/c
; Sequence 1, Application US/09214808A
; Patent No. 6475793
; GENERAL INFORMATION:
;   APPLICANT: Rosenthal, Andre
;   APPLICANT: Freiberg, Christoph
;   APPLICANT: Perret, Xavier Philippe
;   APPLICANT: Broughton, William John
;   TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
;   Patent No. 6475793
;   TITLE OF INVENTION: Plasmid
;   FILE REFERENCE: CARP0068
;   CURRENT APPLICATION NUMBER: US/09/214,808A
;   CURRENT FILING DATE: 1999-06-22
;   PRIOR APPLICATION NUMBER: PCT/IB97/00950
;   PRIOR FILING DATE: 1997-07-10
;   NUMBER OF SEQ ID NOS: 1
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 536165
;   TYPE: DNA
;   ORGANISM: Rhizobium
US-09-214-808-1

Alignment Scores:
Pred. No.:   1.07e+04
Score: 85.00   Length: 536165
Percent Similarity: 37.50%   Matches: 42
Best Local Similarity: 29.17%   Conservative: 12
Query Match: 13.80%   Mismatches: 52
DB: Indels: 38
                                                       Gaps: 6

US-10-659-782A-32 (1-116) x US-09-214-808-1 (1-536165)

Qy   3 SerProGlyThrVal--CysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeuAlaMe 22
              :::||||||||:|| |||||
Db 82810 GCTCCTGGATCCGCCCTTGCTCG------------------TTGCACTGCGCGCC 82775

Qy   22 tAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProProHisLy 42
              |||||||| ::: |||||
Db 82774 GGCTGGATCAGGCGGGCTTCAGACATCTTCCGACCTTGGAAACCGGTTCGCCGCGCA 82715

Qy   42 sAla----------------------------ProHisValProAlaLeuPr 51
              |||| ||
Db 82714 AGCCTTCATGTCTTCGGCCGGGAACCAGATCGCTCGGCCCGATCGGAGCGGCCATTGCC 82655

Qy   51 oLeuSerArgAsnGlnLeuCysAspLeuGlnGlnArgHis----------Trp 65
              ::||| :::|||
Db 82654 GGCCGTAAACACGATCTGTTCATCGGCGCATGCGCAGAACTTCGTGTCGCTGGATCAG 82595

Qy   66 ----------AlaSerValPheSerGlnSerThrLysAspSer----------GlySerAs 79
              ||| :::||| :::|||
Db 82594 CGGTCGAGCGGCCAGTTGCCTTCGAGCGCGTCCCTTGAGGATCCCCTTCGTTTGAAAACTGCG 82535

Qy   79 pLeuThrValSer--GlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProPros 99
              |||||||||||| ||| :::|||
Db 82534 GCTGACCTGGTCGATCCTCGACCGCTGCATGCGCCAAGCCTCGAGATATAGTCCCCCGT 82475

Qy   99 erSerArgGluArgSerHisGlnProSer---------------------CysSerP 114
              ::||| :::|||
Db 82474 CTCCGGATCGTTGATCGCGCAAACGAAATCCAGCTCGCCGCTCTCGAACCATTTGCTCGC 82415

Qy   114 roGluLeu 116
              :::|||
Db 82414 CGGCTGTC 82407

RESULT 10
US-09-252-991A-13395/c
; Sequence 13395, Application US/09252991A

```
;   Patent No. 6551795
;   GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenfield et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;   TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.136
;   CURRENT APPLICATION NUMBER: US/09/252,991A
;   CURRENT FILING DATE: 1999-02-18
;   PRIOR APPLICATION NUMBER: US 60/074,788
;   PRIOR FILING DATE: 1998-02-18
;   PRIOR APPLICATION NUMBER: US 60/094,190
;   PRIOR FILING DATE: 1998-07-27
;   NUMBER OF SEQ ID NOS: 33142
;   SEQ ID NO 13395
;   LENGTH: 867
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13395

Alignment Scores:
Pred. No.:              1.53               Length:            867
Score:                  82.50              Matches:           28
Percent Similarity:     48.65%             Conservative:      8
Best Local Similarity:  37.84%             Mismatches:        28
Query Match:            13.39%             Indels:            11
DB:                                        Gaps:              1

US-10-659-782A-32 (1-116) x US-09-252-991A-13395 (1-867)

Qy    47 ValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGluGlnArgHisTrpAla 66
         ||| ||  :|:|||||  |||            |||  ||| |||||
Db   638 GTCTCCAGTTGCCGGCCAGTTCGGCCACCTGTTCCTGGGTGCGGCCTGGCACTTGGCG 579

Qy    67 SerValPheSerGlnSer------------------------ThrLysAspSerGly 77
         :::::|||  |||                            |||:::|||
Db   578 ACCCTGGCCAGTTCCTCGCGGGCCTGCTCCGCGCTCCGGCGACCAGAAT 519

Qy    78 SerAspLeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPhePro 97
         |||||||||||||| |||  ||||||  ||| |||:::::::
Db   518 TCGGACTTGACTCGCAGTTGCCGGGACTGGGT-CTCCAGCTCCACCAGCGACAGGCGCCA 460

Qy    98 -ProSerArgGluArgSerArgArgSerHisGlnPro 110
          |||||||||||||||||||||
Db   459 GCCGGGGATCGCCTGGTCGAGCAGGCTTTCCCACCAGCCA 420
```

```
RESULT 11
US-09-252-991A-13604/C
;   Sequence 13604, Application US/09252991A
;   Patent No. 6551795
;   GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenfield et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;   TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.136
;   CURRENT APPLICATION NUMBER: US/09/252,991A
;   CURRENT FILING DATE: 1999-02-18
;   PRIOR APPLICATION NUMBER: US 60/074,788
;   PRIOR FILING DATE: 1998-02-18
;   PRIOR APPLICATION NUMBER: US 60/094,190
;   PRIOR FILING DATE: 1998-07-27
;   NUMBER OF SEQ ID NOS: 33142
;   SEQ ID NO 13604
;   LENGTH: 2103
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13604

Alignment Scores:
Pred. No.:              5.7                Length:            2103
Score:                  82.50              Matches:           28
Percent Similarity:     48.65%             Conservative:      8
Best Local Similarity:  37.84%             Mismatches:        28
Query Match:            13.39%             Indels:            11
```

```
DB:                                                Gaps:              1

US-10-659-782A-32 (1-116) x US-09-252-991A-13604 (1-2103)

Qy    47 ValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGluGlnArgHisTrpAla 66
         ||| ||  :|:|||||  |||                  :::
Db   471 GTCTCCAGTTGCCGGCCAGTTCGGCCACCTGTTCCTGGGTGCGGCCTGGCACTTGGCG 412

Qy    67 SerValPheSerGlnSer------------------------ThrLysAspSerGly 77
         :::::|||  |||                            |||:::|||
Db   411 ACCCTGGCCAGTTCCTCGCGGGCCTGCTCCGCGCTCCGGCGACCAGAAT 352

Qy    78 SerAspLeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPhePro 97
         |||||||||||||| |||  ||||||  ||| |||:::::::
Db   351 TCGGACTTGACTCGCAGTTGCCGGGACTGGGT-CTCCAGCTCCACCAGCGACAGGCGCCA 293

Qy    98 -ProSerArgGluArgSerArgArgSerHisGlnPro 110
          |||
Db   292 GCCGGGGATCGCCTGGTCGAGCAGGCTTTCCCACCAGCCA 253
```

```
RESULT 12
US-09-252-991A-13746
;   Sequence 13746, Application US/09252991A
;   Patent No. 6551795
;   GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenfield et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;   TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.136
;   CURRENT APPLICATION NUMBER: US/09/252,991A
;   CURRENT FILING DATE: 1999-02-18
;   PRIOR APPLICATION NUMBER: US 60/074,788
;   PRIOR FILING DATE: 1998-02-18
;   PRIOR APPLICATION NUMBER: US 60/094,190
;   PRIOR FILING DATE: 1998-07-27
;   NUMBER OF SEQ ID NOS: 33142
;   SEQ ID NO 13746
;   LENGTH: 3222
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13746

Alignment Scores:
Pred. No.:              10.8               Length:            3222
Score:                  82.50              Matches:           28
Percent Similarity:     48.65%             Conservative:      8
Best Local Similarity:  37.84%             Mismatches:        28
Query Match:            13.39%             Indels:            11
DB:                                        Gaps:              4

US-10-659-782A-32 (1-116) x US-09-252-991A-13746 (1-3222)

Qy    47 ValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGluGlnArgHisTrpAla 66
         ||| ||  :|:|||||  |||                  :::
Db  2510 GTCTCCAGTTGCCGGCCAGTTCGGCCACCTGTTCCTGGGTGCGGCCTGGCACTTGGCG 2569

Qy    67 SerValPheSerGlnSer------------------------ThrLysAspSerGly 77
         :::::|||  |||                            |||:::|||
Db  2570 ACCCTGGCCAGTTCCTCGCGGGCCTGCTCCGCGCTCCGGCGACCAGAAT 2629

Qy    78 SerAspLeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPhePro 97
         |||||||||||||| |||  ||||||  ||| |||:::::::
Db  2630 TCGGACTTGACTCGCAGTTGCCGGGACTGGGT-CTCCAGCTCCACCAGCGACAGGCGCCA 2688

Qy    98 -ProSerArgGluArgSerArgArgSerHisGlnPro 110
          |||
Db  2689 GCCGGGGATCGCCTGGTCGAGCAGGCTTTCCCACCAGCCA 2728
```

```
RESULT 13
US-08-976-255-2
;   Sequence 2, Application US/08976255
;   Patent No. 6136581
;   GENERAL INFORMATION:
```

APPLICANT: Jono, Keith E.
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: KINASE GENES AND USES
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Lyon & Lyon
  STREET: 633 West Fifth Street
  STREET: Suite 4700
  CITY: Los Angeles
  STATE: California
  COUNTRY: U.S.A.
  ZIP: 90071-2066
COMPUTER READABLE FORM:
  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
  MEDIUM TYPE: storage
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: IBM P.C. DOS 5.0
  SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/976,255
  FILING DATE: No. 6136581ember 21, 1997
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 60/031,675
  FILING DATE: No. 6136581ember 22, 1996
ATTORNEY/AGENT INFORMATION:
  NAME: Warburg, Richard J.
  REGISTRATION NUMBER: 32,327
  REFERENCE/DOCKET NUMBER: 229/182
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (213) 489-1600
  TELEFAX: (213) 955-0440
  TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
  LENGTH: 5267 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
US-08-976-255-2

Alignment Scores:
Pred. No.:   Length: 5267
Score: 29.5   Matches: 37
Percent Similarity: 81.50%   Conservative: 11
Best Local Similarity: 29.27%   Mismatches: 53
Query Match: 22.56%   Indels: 63
DB: 13.23%   Gaps: 6

US-10-659-782A-32 (1-116) x US-08-976-255-2 (1-5267)

Qy   14 GlyMetLeuTrpLeuAspLeuAlaMetAlaGlySer-----------SerPheLeu 28
            |||:|||| ||| ||||| ||:::
Db 4355 GGGCTTTTAGGCTTGCTCGTAGCCCCTGGGGGGCCCTGGAGCCCAGTGGGTGTCTGTAC 4414

Qy   29 SerProGluHisGlnArgValGlnValArgProHisLysAlaProHisValValPro 48
            ||| || |||| :||
Db 4415 ACACATACACACTCAAAAGGGGCCAGTGCCCTGGGCACGGCGGCCCCCCACCCCTGCCC 4474

Qy   49 AlaLeuPro---LeuSerAsnGlnLeuCysAspLeuGluGln--------------- 61
            |||||| |||
Db 4475 TGCCTGCCTGGCCTCGGAGGACCCGCATGCCCCATCCGCAGCTCCTCCGGTGTCTCAC 4534

Qy   62 ---------------GlnArgHisTrpAlaSerValPheSerGln 71
                           ||||||||
Db 4535 AGGACACTTAAACCAGGAGCAGGAGGACGATGGCCAGGTTTGTGAGCCCTCTT 4594

Qy   72 SerThrLysAspSerGlySer------------AspLeuThrValSerGlyArgThrTrp--- 87
            |||:   :::
Db 4595 CCCACCCCCTGCCCCCCACCCCTGCCTGTTCCTGGTGCTCAGGGCAAGGAGAGTGGCCC 4654

Qy   87 ------- 87

Db   4655 TGGGGCCCGTGTCGGTCCGTTCCGCTGCCCTTATCTCAAAGTCCTGGCTGTGTTCCC 4714

Qy   88 ----------------------------GlyLeuArgValLeuAsnArgLeuPhePro 97
                                        |||
Db   4715 CTTCACTGACTCAGTCAGACCCGTAGCCCACCCTTCCCACAGGAACAGGCTGCTCCCA 4774

Qy   98 ProSerSerArg------------------GluArgSerArgSerHisGlnPro 110
             ||| |||||| :::||||||
Db   4775 CCTGGGTCCCGCTGGCCACGGTGGCAGCGCCAAAAGATCAGGGGTGGAGGGGCCTCCA 4834

Qy   111 SerCysSerPro 114
             ||::|||||
Db   4835 GGCTGTACTCCT 4846

RESULT 14
US-09-732-025-3
; Sequence 3, Application US/09732025
; Patent No. 6416990
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001011
; CURRENT APPLICATION NUMBER: US/09/732,025
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 8285
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(8285)
; OTHER INFORMATION: n = A,T,C or G
US-09-732-025-3

Alignment Scores:
Pred. No.:   Length: 8285
Score: 66.4   Matches: 36
Percent Similarity: 81.00%   Conservative: 12
Best Local Similarity: 37.21%   Mismatches: 46
Query Match: 27.91%   Indels: 36
DB: 13.15%   Gaps: 4

US-10-659-782a-32 (1-116) x US-09-732-025-3 (1-8285)

Qy   1 MetProSerProGlyThrValCysSer----------------LeuLeuLeuLeuGly 14
            :::|| ||||||| ||::||
Db 6017 CTCCCCAAGCCAGGCACACC-TGCACAAACCAGAGCCGACCCTCCAGCTGCCTTCTAGGA 6075

Qy   15 MetLeuTrpLeuAspLeuAlaMetAlaGlySerSerPheLeuSerProGluHisGlnArg 34
Db 6076 CACCTG-- 6081

Qy   35 ValGlnValArgProHisLysAlaProHisValValProAlaLeuProLeuSerAsn 54
            :::|||||| ||| |||::||
Db 6082 ------TGCAGGGGTCCCAGACCCAGGCAGCCATGACCCTGCCGAGC 6135

Qy   55 GlnLeuCysAspLeu------------------GluGlnGlnArgHisTrpAlaSerVal 68
            :::||||| ||| :::::|
Db 6136 ACGGTTGTGATCTTTGCTGGCCGCCACGGGAGCAGCATGGCCCGGGCCCCTTCTGCCTGT 6195

Qy   69 PheSerGlnSerThrLysAspSerGlySerAspLeuThrValSerGlyArgThrTrpGly 88
            |||||||||
Db 6196 GCTGCCAACTATGCCAGCATTCGGTTCCTGACCCTGGGGTTGACCCACTGACCCCGGGGG 6255

Qy   89 LeuArgValLeuAsnArgLeuPheProProSerSerArgGluArgSerArg---------- 105
            ||| |||||||::||
Db 6256 TTGACCCACTGACCCCACAGAGTCCCCCCTGCAGCCAGCCAGAACGTTCCCAGGCAGAACTC 6315

Qy   106 ArgSerHisGlnProSerCysSerPro 114

```
Db        6316 CGCTCCCCTGCTCCAAACTGCTCTCCT 6342
               ||||||        |||::|||||||||
```

RESULT 15
US-09-739-455-3
; Sequence 3, Application US/09739455
; Patent No. 6413756
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000653
; CURRENT APPLICATION NUMBER: US/09/739,455
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 11827
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(11827)
; OTHER INFORMATION: n = A,T,C or G
US-09-739-455-3

Alignment Scores:
Pred. No.:   113   Length: 11827
Score: 81.00   Matches: 36
Percent Similarity: 37.21%   Conservative: 12
Best Local Similarity: 27.91%   Mismatches: 46
Query Match: 13.15%   Indels: 36
DB: 4   Gaps: 4

US-10-659-782A-32. (1-116) x US-09-739-455-3 (1-11827)

Qy   1 MetProSerProGlyThrValCysSer-------------LeuLeuLeuLeuGly 14
         :::|||| |||||||||| |||::: ||||||||||
Db 7868 CTCCCCAAGCCAGGCACACC-TGCACAAACCCAGAGCCGACCCTCAGCTGCCTTCTAGGA 7926

Qy   15 MetLeuTrpLeuAspLeuAlaMetAlaGlySerSerPheLeuSerProGluHisGlnArg 34
         |||
Db 7927 CACCTG-- 7932

Qy   35 ValGlnValArgProHisLysAlaProHisValValProAlaLeuProLeuSerAsn 54
         ||| |||::: ||| ::::
Db 7933 ------TGCAGGGTCCGAGCCCCAGGCCCCAGAGCAGCCCATGACCCTGCCGAGC 7986

Qy   55 GlnLeuCysAspLeu------------GluGlnIleArgHisTrpAlaSerVal 68
         :::|||||||||| ||| :::::::
Db 7987 ACGGTGTGTGATCTTTGCTGGCCGCCCACGCGGAGCATGGCCCGGGCCCCTTCTGCCTGT 8046

Qy   69 PheSerGlnSerThrLysAspSerGlySerAspLeuThrValSerGlyArgThrTrpGly 88
         ::: ||| ||| ||| ||| || |||
Db 8047 GCTGCCAACTATGCGCAGCATTCGGTTCCTGACCCTGGGGTTGACCCACTGACCCCGGGG 8106

Qy   89 LeuArgValLeuAsnArgLeuPheProProSerSerArgGluArgSerArg--------- 105
         ||| |||:::: ||||||:::
Db 8107 TTGACCCACTGACCCCCACAGAGTCCCCCGTGCAGCCAAGAACGTTCCCAGGCAGAGACTC 8166

Qy   106 ArgSerHisGlnProSerCysSerPro 114
         ||| ||:::||||||||||
Db 8167 CGCTCCCCTGCTCCAAACTGCTCTCCT 8193
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Search completed: February 10, 2005, 16:02:43
Job time : 181 secs

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             Copyright   GenCore version 5.1.6
                         (c) 1993 - 2005  Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:      February 10, 2005, 14:15:44 ; Search time 467 Seconds
                                          (without alignments)
                                          1427.244 Million cell updates/sec

Title:          US-10-659-782A-32
Perfect score:  616
Sequence:       1 MPSPGTVCSLLLGMLWLDL.........PPSSRERSRRSHQPSCSPEL 116

Scoring table:  BLOSUM62

                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters:      8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US10659782/runat_05022005_161919_4325/app_query.fasta_1.263
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10659782 @CGN_1_1_480 @runat_05022005_161919_4325
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
  1:  /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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  3:  /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
  4:  /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
  5:  /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
  6:  /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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 10:  /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
 11:  /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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 13:  /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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 21:  /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

                              SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Result No.	Score	Query Match %	Length	DB	ID	Description
1	220	35.7	447	15	US-10-294-191A-11	Sequence 11, Appl
2	214	34.7	351	12	US-09-794-987-1	Sequence 1, Appli
3	214	34.7	351	15	US-09-796-158-1	Sequence 1, Appli
4	214	34.7	351	15	US-10-186-414-3	Sequence 3, Appli
5	214	34.7	351	15	US-10-607-706-1	Sequence 1, Appli
6	214	34.7	351	18	US-10-679-813-1	Sequence 1, Appli
7	214	34.7	401	17	US-10-477-506-3	Sequence 3, Appli
8	214	34.7	510	17	US-10-477-506-4	Sequence 4, Appli
9	214	34.7	511	15	US-10-191-997-112	Sequence 112, App
10	214	34.7	527	9	US-09-853-253-1	Sequence 1, Appli
11	214	34.7	596	13	US-10-098-841-252	Sequence 252, App
12	214	34.7	654	9	US-09-989-722-267	Sequence 267, App
13	214	34.7	654	9	US-09-989-723-267	Sequence 267, App
14	214	34.7	654	9	US-09-989-279-267	Sequence 267, App
15	214	34.7	654	9	US-09-989-727-267	Sequence 267, App
16	214	34.7	654	9	US-09-989-731-267	Sequence 267, App
17	214	34.7	654	9	US-09-989-732-267	Sequence 267, App
18	214	34.7	654	9	US-09-991-073-267	Sequence 267, App
19	214	34.7	654	9	US-09-990-442-267	Sequence 267, App
20	214	34.7	654	9	US-09-991-163-267	Sequence 267, App
21	214	34.7	654	9	US-09-993-604-267	Sequence 267, App
22	214	34.7	654	9	US-09-990-456-267	Sequence 267, App
23	214	34.7	654	9	US-09-989-721-267	Sequence 267, App
24	214	34.7	654	9	US-09-992-598-267	Sequence 267, App
25	214	34.7	654	9	US-09-989-293A-267	Sequence 267, App
26	214	34.7	654	9	US-09-989-735-267	Sequence 267, App
27	214	34.7	654	9	US-09-990-444-267	Sequence 267, App
28	214	34.7	654	9	US-09-991-181-267	Sequence 267, App
29	214	34.7	654	9	US-09-989-730-267	Sequence 267, App
30	214	34.7	654	9	US-09-990-436-267	Sequence 267, App
31	214	34.7	654	9	US-09-993-687-267	Sequence 267, App
32	214	34.7	654	10	US-09-989-734-267	Sequence 267, App
33	214	34.7	654	10	US-09-997-653-267	Sequence 267, App
34	214	34.7	654	10	US-09-989-724-267	Sequence 267, App
35	214	34.7	654	10	US-09-989-728-267	Sequence 267, App
36	214	34.7	654	10	US-09-990-441-267	Sequence 267, App
37	214	34.7	654	10	US-09-993-667-267	Sequence 267, App
38	214	34.7	654	10	US-09-997-428-267	Sequence 267, App
39	214	34.7	654	10	US-09-997-666-267	Sequence 267, App
40	214	34.7	654	10	US-09-990-438-267	Sequence 267, App
41	214	34.7	654	10	US-09-990-562-267	Sequence 267, App
42	214	34.7	654	10	US-09-990-711-267	Sequence 267, App
43	214	34.7	654	10	US-09-989-726-267	Sequence 267, App
44	214	34.7	654	10	US-09-998-156-267	Sequence 267, App
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ALIGNMENTS

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RESULT 1
US-10-294-191A-11
; Sequence 11, Application US/10294191A
; Publication No. US20030211512A1
; GENERAL INFORMATION:
;  APPLICANT: Rothschild, Max F.
;  APPLICANT: Kim, Kwan Suk
;  APPLICANT: Anderson, Lloyd L.
;  TITLE OF INVENTION: Novel Ghrelin Alleles and Use of the Same for Genetically Typing
;  FILE REFERENCE: P05408US1
;  CURRENT APPLICATION NUMBER: US/10/294,191A
;  CURRENT FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: US 60/333,222
;  PRIOR FILING DATE: 2001-11-14
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 11
;  LENGTH: 447
;  TYPE: DNA
;  ORGANISM: Porcine
US-10-294-191A-11
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Alignment Scores:
Pred. No.:                3.29e-18          Length:                447
Score:                    220.00            Matches:               65
Percent Similarity:       57.81%            Conservative:          9
Best Local Similarity:    50.78%            Mismatches:            36
Query Match:              35.71%            Indels:                18
DB:                                         Gaps:                  5

US-10-659-782A-32 (1-116) x US-10-294-191A-11 (1-447)

Qy     1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeu--Asp 19
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Db    11 ATGCCCTCCACGGGACCATTTGCAGCCTGCTCCTCAGCGTGCTCCTCATGGCAGAC 70

Qy    20 LeuAlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgPro 39
           |||||||||||||||||||||||| |||||||||  |||:: ||| || :|||||||
Db    71 TTGGCCATGGCGGGCTCCAGCTTCTTGAGCCCTGAACACCCAGAAAGTCAGGTAAGACGT 130

Qy    40 ProHisLysAlaPro---------HisValProAlaLeuProLeuSerArgAsnGln 55
           :::|||||||  |              ::|||::|||||||| ||||:|:|
Db   131 CTCCCCAGAGCCCCGGCTTCTGCGGGTACCTCATCCCAGCCCTTCCATGAGTTGGGACC 190

Qy    56 LeuCysAspLeuGluGluGlnArgHisTrpAlaSerValPheSerGlnSer--ThrLysA 75
           ||| :::                   :|    |||    ||| :|||
Db   191 TGGGCTCACCTG--------------CTCTGGGCTTCAGGCCTCCCAAGGAGGACTCTGG 238

Qy    75 Sp---SerGlySerAspLeuThrVal-------SerGlyArgThrTrpG 88
           :||||        |||  ||||||       |||
Db   239 ATCTGCAAGGGAGCCCATACCTTGCTCTTGCTTCTCGGAAGGAAGTAGTGGGGGGTGGG 298

Qy    88 lyLeuArgValLeuAsnArgLeuPheProProSerSerArgGluArgSerArgArgSerH 108
             ||:||          |||||||||||| ||||||||       |||
Db   299 CATCTTAGGGCCTCAAGAGAGCAGTTCCTCTTTCCAGAGAGAAAGGAGTCCAAGAAGCC 358

Qy   108 isGlnProSerCysSerPro 114
           |||||:::  |||||
Db   359 AGCAGCCAAACTGAAGCCCC 378

RESULT 2
US-09-794-987-1
; Sequence 1, Application US/09794987
; Patent No. US2001041791A1
; GENERAL INFORMATION:
     APPLICANT: Sheppard, Paul O.
              Deisher, Theresa A.
     TITLE OF INVENTION: MOTILIN HOMOLOGS
     NUMBER OF SEQUENCES: 7
     CORRESPONDENCE ADDRESS:
         ADDRESSEE: ZymoGenetics, Inc.
         STREET: 1201 Eastlake Avenue East
         CITY: Seattle
         STATE: WA
         COUNTRY: USA
         ZIP: 98102
     COMPUTER READABLE FORM:
         MEDIUM TYPE: Diskette
         COMPUTER: IBM Compatible
         OPERATING SYSTEM: DOS
         SOFTWARE: FastSEQ for Windows Version 2.0
     CURRENT APPLICATION DATA:
         APPLICATION NUMBER: US/09/794,987
         FILING DATE: 27-Feb-2001
         CLASSIFICATION: <Unknown>
     PRIOR APPLICATION DATA:
         APPLICATION NUMBER: 09/046,479
         FILING DATE: <Unknown>
     ATTORNEY/AGENT INFORMATION:
         NAME: Sawislak, Deborah A
         REGISTRATION NUMBER: 37,438
         REFERENCE/DOCKET NUMBER: 97-04
     TELECOMMUNICATION INFORMATION:
         TELEPHONE: 206-442-6672
```

```
                       TELEFAX: 206-442-6678
                       TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
     SEQUENCE CHARACTERISTICS:
         LENGTH: 351 base pairs
         TYPE: nucleic acid
         STRANDEDNESS: single
         TOPOLOGY: linear
     MOLECULE TYPE: cDNA
     FEATURE:
         NAME/KEY: sig_peptide
         LOCATION: 1..351
         OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-794-987-1

Alignment Scores:
Pred. No.:                1.39e-17          Length:                351
Score:                    214.00            Matches:               51
Percent Similarity:       44.44%            Conservative:          1
Best Local Similarity:    43.59%            Mismatches:            0
Query Match:              34.74%            Indels:                65
DB:                                         Gaps:                  9

US-10-659-782A-32 (1-116) x US-09-794-987-1 (1-351)

Qy     1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
           ||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG 60

Qy    21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG--------- 108

Qy    41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   108 ------------------------------------------------------------ 108

Qy    61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   108 ------------------------------------------------------------ 108

Qy    81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   108 ------------------------------------------------------------ 108

Qy   101 ArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
           :::  ||||||||||||||||||||||||||||||||
Db   109 CAGAGAAAGGAGTCCAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157

RESULT 3
US-09-796-158-1
; Sequence 1, Application US/09796158
; Publication No. US2004025345A1
; GENERAL INFORMATION:
     APPLICANT: Sheppard, Paul O.
              Deisher, Theresa A.
     TITLE OF INVENTION: MOTILIN HOMOLOGS
     NUMBER OF SEQUENCES: 7
     CORRESPONDENCE ADDRESS:
         ADDRESSEE: ZymoGenetics, Inc.
         STREET: 1201 Eastlake Avenue East
         CITY: Seattle
         STATE: WA
         COUNTRY: USA
         ZIP: 98102
     COMPUTER READABLE FORM:
         MEDIUM TYPE: Diskette
         COMPUTER: IBM Compatible
         OPERATING SYSTEM: DOS
         SOFTWARE: FastSEQ for Windows Version 2.0
     CURRENT APPLICATION DATA:
         APPLICATION NUMBER: US/09/796,158
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FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/046,479
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1...351
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-796-158-1

Alignment Scores:
Pred. No.:   1.39e-17   Length: 351
Score: 214.00   Matches: 51
Percent Similarity: 44.44%   Conservative: 1
Best Local Similarity: 43.59%   Mismatches: 0
Query Match: 34.74%   Indels: 65
DB: 12   Gaps: 1

US-10-659-782A-32 (1-116) x US-09-796-158-1 (1-351)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu   20
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Db   1 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCGGCATGGTCTGGCTGGACTTG   60

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro   40
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCATGGCAGGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGTCCAG----------- 108

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu   60
Db 108 -- 108

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu   80
Db 108 -- 108

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db 108 -- 108

Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
         ::: ||||||||||||||||||||||||||||||||||||||||||||||
Db 109 CAGAGAAAGGAGTCGAAGAGCCAAGCTGCAGCCCCGAGCTC 157

RESULT 4
US-10-186-414-3
; Sequence 3, Application US/10186414
; Publication No. US20030176640A1
; GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Deisher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: SGIP PEPTIDES
FILE REFERENCE: 99-51
CURRENT APPLICATION NUMBER: US/10/186,414

CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US/09/608,810
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/141,592
PRIOR FILING DATE: 1999-06-30
SOFTWARE: FastSEQ for Windows Version 3.0
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 3
LENGTH: 351
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(351)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (1)...(69)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (70)...(351)
US-10-186-414-3

Alignment Scores:
Pred. No.:   1.39e-17   Length: 351
Score: 214.00   Matches: 51
Percent Similarity: 44.44%   Conservative: 1
Best Local Similarity: 43.59%   Mismatches: 0
Query Match: 34.74%   Indels: 65
DB: 15   Gaps: 1

US-10-659-782A-32 (1-116) x US-10-186-414-3 (1-351)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu   20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCGGCATGGTCTGGCTGGACTTG   60

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro   40
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCATGGCAGGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGTCCAG----------- 108

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu   60
Db 108 -- 108

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu   80
Db 108 -- 108

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db 108 -- 108

Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
         ::: ||||||||||||||||||||||||||||||||||||||||||||||
Db 109 CAGAGAAAGGAGTCGAAGAGCCAAGCTGCAGCCCCGAGCTC 157

RESULT 5
US-10-607-706-1
; Sequence 1, Application US/10607706
; Publication No. US2003023S887A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: TML Polynucleotides
FILE REFERENCE: 97-04D3
CURRENT APPLICATION NUMBER: US/10/607,706
CURRENT FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 09/404,417
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/046,479
PRIOR FILING DATE: 1998-03-28

; PRIOR APPLICATION NUMBER: 60/041,102
; PRIOR FILING DATE: 1997-03-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(351)
US-10-607-706-1

Alignment Scores:
Pred. No.:
Score: 1.39e-17   Length: 351
Percent Similarity: 214.00   Matches: 51
Best Local Similarity: 44.44%   Conservative: 1
Query Match: 43.59%   Mismatches: 0
DB: 34.74%   Indels: 65
                          15   Gaps: 1

US-10-659-782A-32 (1-116) x US-10-607-706-1 (1-351)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG 60

Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnArgValArgProPro 40
        |||||||||||||||||||||||||||||||||||||
Db 61 GCCATGGCAGGTTCCAGCTTCCTGAGCCCTGAACACCAGAGTCCAG----------- 108

Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 108 ----------------- 108

Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 108 ----------------- 108

Qy 81 ThrValSerGlyArgThrTrpLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db 108 ----------------- 108

Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
        :::||||||||||||||||||||||||||||||||||
Db 109 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157

RESULT 6
US-10-679-813-1
; Sequence 1, Application US/10679813
; Publication No. US20040208866A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN R.
; APPLICANT: SHEPPARD, PAUL O.
; APPLICANT: BISHOP, PAUL D.
; APPLICANT: KUIJPER JOSEPH L.
; APPLICANT: DEISHER, THERESA A.
; TITLE OF INVENTION: METHODS OF REGULATING BODY WEIGHT
; FILE REFERENCE: 02-23
; CURRENT APPLICATION NUMBER: US/10/679,813
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/416,918
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(351)
US-10-679-813-1

Alignment Scores:
Pred. No.:
Score: 1.39e-17   Length: 351
Percent Similarity: 214.00   Matches: 51
Best Local Similarity: 44.44%   Conservative: 1
Query Match: 43.59%   Mismatches: 0
DB: 34.74%   Indels: 65
                          18   Gaps: 1

US-10-659-782A-32 (1-116) x US-10-679-813-1 (1-351)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTG 60

Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnArgValArgProPro 40
        |||||||||||||||||||||||||||||||||||||
Db 61 GCCATGGCAGGTTCCAGCTTCCTGAGCCCTGAACACCAGAGTCCAG----------- 108

Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 108 ----------------- 108

Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 108 ----------------- 108

Qy 81 ThrValSerGlyArgThrTrpLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db 108 ----------------- 108

Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
        :::||||||||||||||||||||||||||||||||||
Db 109 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157

RESULT 7
US-10-477-506-3
; Sequence 3, Application US/10477506
; Publication No. US20040157227A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Lisa K
; APPLICANT: Jeffery, Penelope L
; APPLICANT: Herington, Adrian C
; TITLE OF INVENTION: REPRODUCTIVE CANCER DIAGNOSIS AND THERAPY
; FILE REFERENCE: 225181
; CURRENT APPLICATION NUMBER: US/10/477,506
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: PR9567
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: PR4919
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: PCT/AU02/000582
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-506-3

Alignment Scores:
Pred. No.:
Score: 1.64e-17   Length: 401
Percent Similarity: 214.00   Matches: 51
Best Local Similarity: 44.44%   Conservative: 1
Query Match: 43.59%   Mismatches: 0
DB: 34.74%   Indels: 65
                          17   Gaps: 1

US-10-659-782A-32 (1-116) x US-10-477-506-3 (1-401)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100

Db   140 ------

Qy   101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
           ::: |||||||||||||||||||||||||||||||||||||||||
Db   141 CAGAGAAAGAGAGTCGAAGAAGCACCAGCCAAGCTGCAGCCCCGAGCTC 189

RESULT 9
US-10-191-997-112
; Sequence 112, Application US/10191997
; Publication No. US2003020783A1
; GENERAL INFORMATION:
; APPLICANT: Oligos Etc., Inc.
; APPLICANT: DALE, Roderic M. K.
; APPLICANT: ARROW, Amy
; APPLICANT: THOMPSON, Terry
; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their
; FILE REFERENCE: 54800-5019
; CURRENT APPLICATION NUMBER: US/10/191,997
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,820
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 112
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: NM_016362
US-10-191-997-112

Alignment Scores:
Pred. No.:   Length: 511
Score: 2.2e-17   Matches: 51
Percent Similarity: 214.00   Conservative: 1
Best Local Similarity: 44.44%   Mismatches: 0
Query Match: 43.59%   Indels: 65
DB: 34.74%   Gaps: 1
                    15

US-10-659-782A-32 (1-116) x US-10-191-997-112 (1-511)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   34 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCGCTCCTCGGCCATGCTCTGGCTGGACTTG 93

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   94 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG----------- 141

Qy   41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db   141 ------ 141

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db   141 ------ 141

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db   141 ------ 141

Qy   101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
           ::: |||||||||||||||||||||||||||||||||||||||||
Db   142 CAGAGAAAGAGAGTCGAAGAAGCACCAGCCAAGCTGCAGCCCCGAGCTC 190

RESULT 10
US-09-853-253-1
; Sequence 1, Application US/09853253
; Patent No. US20020055156A1

Db   33 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCGCTCCTCGGCCATGCTCTGGCTGGACTTG 92

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   93 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG----------- 140

Qy   41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db   140 ------ 140

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db   140 ------ 140

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db   140 ------ 140

Qy   101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
           ::: |||||||||||||||||||||||||||||||||||||||||
Db   141 CAGAGAAAGAGAGTCGAAGAAGCACCAGCCAAGCTGCAGCCCCGAGCTC 189

RESULT 8
US-10-477-506-4
; Sequence 4, Application US/10477506
; Publication No. US20040157227A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Lisa K
; APPLICANT: Jeffery, Penelope L
; APPLICANT: Herington, Adrian C
; TITLE OF INVENTION: REPRODUCTIVE CANCER DIAGNOSIS AND THERAPY
; FILE REFERENCE: 225181
; CURRENT APPLICATION NUMBER: US/10/477,506
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: PR9567
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: PR4919
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: PCT/AU02/000582
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-506-4

Alignment Scores:
Pred. No.:   Length: 510
Score: 2.19e-17   Matches: 51
Percent Similarity: 214.00   Conservative: 1
Best Local Similarity: 44.44%   Mismatches: 0
Query Match: 43.59%   Indels: 65
DB: 34.74%   Gaps: 1
                    17

US-10-659-782A-32 (1-116) x US-10-477-506-4 (1-510)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   33 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCGCTCCTCGGCCATGCTCTGGCTGGACTTG 92

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   93 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG----------- 140

Qy   41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db   140 ------ 140

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db   140 ------ 140

; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)...(400)
US-09-853-253-1

Alignment Scores:
Pred. No.:   2.28e-17
Score: 214.00
Percent Similarity: 44.44%
Best Local Similarity: 43.59%
Query Match: 34.74%
DB:

Length: 527
Matches: 51
Conservative: 1
Mismatches: 0
Indels: 65
Gaps: 9

US-10-659-782A-32 (1-116) x US-09-853-253-1 (1-527)

Qy   1 MetProSerGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   50 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTCGGCCATGCTCCTCGGCTGGACTTG 109

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnArgProPro 40
        |||||||||||||
Db 110 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAGCACCAGAGAGTCCAG---------- 157

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60

Db 157 -- 157

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80

Db 157 -- 157

Qy   81 ThrValSerGlyArgThrGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100

Db 157 -- 157

Qy 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
        ||| |||||||||||||||||||||||||||||||||||||||
Db 158 CAGAGAAAGGAGTCGAAGAAGCCACCAGCAAGCTGCAGCCCCGAGCTC 206

RESULT 11
US-10-098-841-252
; Sequence 252, Application US/10098841
; Publication No. US20020197679A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei

; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020197679A1e1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2
; CURRENT APPLICATION NUMBER: US/10/098,841
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: pt_Fl_genes Version 1.0
; SEQ ID NO 252
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (111)..(464)
US-10-098-841-252

Alignment Scores:
Pred. No.:   2.65e-17
Score: 214.00
Percent Similarity: 44.44%
Best Local Similarity: 43.59%
Query Match: 34.74%
DB:

Length: 596
Matches: 51
Conservative: 1
Mismatches: 0
Indels: 65
Gaps: 1

US-10-659-782A-32 (1-116) x US-10-098-841-252 (1-596)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 111 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTCGGCCATGCTCCTCGGCTCTGGACTTG 170

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnArgProPro 40
        ||||||||||||
Db 171 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG----------- 218

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60

Db 218 -- 218

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80

Db 218 -- 218

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100

Db 218 -- 218

Qy 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
        ||| |||||||||||||||||||||||||||||||||||||||
Db 219 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 267

RESULT 12
US-09-989-722-267
; Sequence 267, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul J.
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Gurney,Austin L.
APPLICANT: Kljavin,Ivar J.
APPLICANT: Napier,Mary A.
APPLICANT: Pan,James
APPLICANT: Paoni,Nicholas F.
APPLICANT: Roy,Margaret Ann
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24

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Qy      101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
            ::: |||||||||||||||||||||||||||||||||||||||||||
Db      284 CAGAGAAAGGAGTCGAAGAGCCACCAGCCAAGCTGCAGCCCGAGCTC 332
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RESULT 13
US-09-989-723-267
; Sequence 267, Application US/09989723
; Patent No. US2002007092A1
; GENERAL INFORMATION:
;   APPLICANT: Ashkenazi,Avi J.
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Botstein,David
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Eaton,Dan L.
;   APPLICANT: Ferrara,Napoleone
;   APPLICANT: Fong,Sherman
;   APPLICANT: Gerber,Hanspeter
;   APPLICANT: Gerritsen,Mary E.
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Grimaldi,J.Christopher
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Kljavin,Ivar J.
;   APPLICANT: Napier,Mary A.
;   APPLICANT: Pan,James
;   APPLICANT: Paoni,Nicholas F.
;   APPLICANT: Roy, Margaret Ann
;   APPLICANT: Stewart, Timothy A.
;   APPLICANT: Tumas, Daniel
;   APPLICANT: Watanabe, Colin K.
;   APPLICANT: Williams, P. Mickey
;   APPLICANT: Wood, William I.
;   APPLICANT: Zhang, Zemin
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION: Acids Encoding the Same
;   FILE REFERENCE: P2730P1C62
;   CURRENT APPLICATION NUMBER: US/09/989,723
;   CURRENT FILING DATE: 2001-11-19
;   PRIOR APPLICATION NUMBER: 60/049787
;   PRIOR FILING DATE: 1997-06-16
;   PRIOR APPLICATION NUMBER: 60/062250
;   PRIOR FILING DATE: 1997-10-17
;   PRIOR APPLICATION NUMBER: 60/065186
;   PRIOR FILING DATE: 1997-11-12
;   PRIOR APPLICATION NUMBER: 60/065311
;   PRIOR FILING DATE: 1997-11-13
;   PRIOR APPLICATION NUMBER: 60/066770
;   PRIOR FILING DATE: 1997-11-24
;   PRIOR APPLICATION NUMBER: 60/075945
;   PRIOR FILING DATE: 1998-02-25
;   PRIOR APPLICATION NUMBER: 60/078910
;   PRIOR FILING DATE: 1998-03-20
;   PRIOR APPLICATION NUMBER: 60/083322
;   PRIOR FILING DATE: 1998-04-28
;   PRIOR APPLICATION NUMBER: 60/084600
;   PRIOR FILING DATE: 1998-05-07
;   PRIOR APPLICATION NUMBER: 60/087106
;   PRIOR FILING DATE: 1998-05-28
;   PRIOR APPLICATION NUMBER: 60/087607
;   PRIOR FILING DATE: 1998-06-02
;   PRIOR APPLICATION NUMBER: 60/087609
;   PRIOR FILING DATE: 1998-06-02
;   PRIOR APPLICATION NUMBER: 60/087759
;   PRIOR FILING DATE: 1998-06-02
;   PRIOR APPLICATION NUMBER: 60/087827
;   PRIOR FILING DATE: 1998-06-03
;   PRIOR APPLICATION NUMBER: 60/088021
;   PRIOR FILING DATE: 1998-06-04
;   PRIOR APPLICATION NUMBER: 60/088025
;   PRIOR FILING DATE: 1998-06-04
;   PRIOR APPLICATION NUMBER: 60/088026
;   PRIOR FILING DATE: 1998-06-04
;   PRIOR FILING DATE: 1998-06-24
;   PRIOR APPLICATION NUMBER: 60/090535
;   PRIOR FILING DATE: 1998-06-24
;   PRIOR APPLICATION NUMBER: 60/090540
;   PRIOR FILING DATE: 1998-06-24
;   PRIOR APPLICATION NUMBER: 60/090542
;   PRIOR FILING DATE: 1998-06-24
;   PRIOR APPLICATION NUMBER: 60/090557
;   PRIOR FILING DATE: 1998-06-24
;   PRIOR APPLICATION NUMBER: 60/090676
;   PRIOR FILING DATE: 1998-06-25
;   PRIOR APPLICATION NUMBER: 60/090678
;   PRIOR FILING DATE: 1998-06-25
;   PRIOR APPLICATION NUMBER: 60/090690
;   PRIOR FILING DATE: 1998-06-25
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;   PRIOR APPLICATION NUMBER: 60/090695
;   PRIOR FILING DATE: 1998-06-25
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;   PRIOR FILING DATE: 1998-07-07
;   PRIOR APPLICATION NUMBER: 60/092182
;   PRIOR FILING DATE: 1998-07-09
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Alignment Scores:
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Score:                  214.00            Matches:         51
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Best Local Similarity:  43.59%            Mismatches:      0
Query Match:            34.74%            Indels:          65
DB:                     9                 Gaps:            1
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US-10-659-782A-32 (1-116) x US-09-989-722-267 (1-654)

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Qy   21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
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Db  236 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG---------- 283

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysLeuAspGlu 60
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Db  283 ------------------------------------------------------------ 283

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
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Db  283 ------------------------------------------------------------ 283

Qy   81 ThrValSerGlyArgThrTrpLeuArgValLeuAsnArgLeuPheProProSerSer 100
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Db  283 ------------------------------------------------------------ 283
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PRIOR APPLICATION NUMBER: 60/091633 PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978 PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982 PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182 PRIOR FILING DATE: 1998-07-09

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Best Local Similarity: 44.44%   Mismatches: 0
Query Match: 43.59%   Indels: 65
DB: 34.74%   Gaps: 1

US-10-659-782A-32 (1-116) x US-09-989-723-267 (1-654)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

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Qy     21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro   40
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Db    236 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG------------- 283
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Qy     41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu   60

Db    283 ------------------------------------------------------------- 283

Qy     61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu   80

Db    283 ------------------------------------------------------------- 283

Qy     81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuAsnArgLeuPheProProSer  100

Db    283 ------------------------------------------------------------- 283

Qy    101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
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; Sequence 267, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
;   APPLICANT: Ashkenazi,Avi J.
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Botstein,David
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Eaton,Dan L.
;   APPLICANT: Ferrara,Napoleone
;   APPLICANT: Fong,Sherman
;   APPLICANT: Gerber,Hanspeter
;   APPLICANT: Gerritsen,Mary E.
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Grimaldi,J.Christopher
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Kljavin,Ivar J.
;   APPLICANT: Napier,Mary A.
;   APPLICANT: Pan,James
;   APPLICANT: Paoni,Nicholas F.
;   APPLICANT: Roy, Margaret Ann
;   APPLICANT: Stewart, Timothy A.
;   APPLICANT: Tumas, Daniel
;   APPLICANT: Watanabe, Colin K.
;   APPLICANT: Williams, P. Mickey
;   APPLICANT: Wood, William I.
;   APPLICANT: Zhang, Zemin
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION: Acids Encoding the Same
;   FILE REFERENCE: P2730P1C56
;   CURRENT APPLICATION NUMBER: US/09/989,279
;   CURRENT FILING DATE: 2001-11-19
;   PRIOR APPLICATION NUMBER: 60/049787
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;   PRIOR FILING DATE: 1998-04-28
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;   PRIOR FILING DATE: 1998-06-17
;   PRIOR APPLICATION NUMBER: 60/089600

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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.:              2.97e-17          Length:        654
Score:                  214.00            Matches:        51
Percent Similarity:     44.44%            Conservative:   0
Best Local Similarity:  43.59%            Mismatches:     0
Query Match:            34.74%            Indels:        65
DB:                                       Gaps:           1

US-10-659-782A-32 (1-116) x US-09-989-279-267 (1-654)

Qy    1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu  20
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Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro  40
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  236 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG-----------  283

Qy   41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu  60
Db  283 -----------------------------------------------------------  283

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu  80
Db  283 -----------------------------------------------------------  283

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db  283 -----------------------------------------------------------  283

Qy  101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
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; GENERAL INFORMATION:
; APPLICANT:    Ashkenazi, Avi J.
; APPLICANT:    Baker, Kevin P.
; APPLICANT:    Botstein, David
; APPLICANT:    Desnoyers, Luc
; APPLICANT:    Eaton, Dan L.
; APPLICANT:    Ferrara, Napoleone
; APPLICANT:    Fong, Sherman
; APPLICANT:    Gerber, Hanspeter
; APPLICANT:    Gerritsen, Mary E.
; APPLICANT:    Godard, Audrey
; APPLICANT:    Godowski, Paul J.
; APPLICANT:    Grimaldi, J.Christopher
; APPLICANT:    Gurney, Austin L.
; APPLICANT:    Kljavin, Ivar J.
; APPLICANT:    Napier, Mary A.
; APPLICANT:    Pan, James
; APPLICANT:    Paoni, Nicholas F.
; APPLICANT:    Roy, Margaret Ann
; APPLICANT:    Stewart, Timothy A.
; APPLICANT:    Tumas, Daniel
; APPLICANT:    Watanabe, Colin K.
; APPLICANT:    Williams, P. Mickey
; APPLICANT:    Wood, William I.
; APPLICANT:    Zhang, Zemin
; TITLE OF INVENTION:  Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION:  Acids Encoding the Same
; FILE REFERENCE: P2730P1C65
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PRIOR APPLICATION NUMBER: 60/089599
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PRIOR APPLICATION NUMBER: 60/089801
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25

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PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
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PRIOR APPLICATION NUMBER: 60/091360
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PRIOR APPLICATION NUMBER: 60/091478
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PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Alignment Scores:
Pred. No.:                           2.97e-17          Length:          654
Score:                               214.00            Matches:         51
Percent Similarity:                  44.44%            Conservative:    1
Best Local Similarity:               43.59%            Mismatches:      0
Query Match:                         34.74%            Indels:          65
                                     9                 Gaps:            1
DB:
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US-10-659-782A-32 (1-116) x US-09-989-727-267 (1-654)

Qy    1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  176 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCCGGCATGCTCTGGCTGGACTTG 235

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db  236 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG------------ 283

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuProLeuCysAspLeuCysLeuGlu 60
Db  283 ---------------------------------------------------------------------- 283

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db  283 ---------------------------------------------------------- 283

Qy   81 ThrValSerGlyArgThrTrpLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db  283 -------------------------------------------------------- 283

Qy  101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
          :::    ||||||||||||||||||||||||||||||||||||||||||
Db  284 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCACCAAGCTCCAGCCCCGAGCTC 332
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Search completed: February 10, 2005, 16:09:05
Job time : 472 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 10, 2005, 13:45:44 ; Search time 2546 Seconds
                                               (without alignments)
                                               1660.255 Million cell updates/sec

Title: US-10-659-782A-32
Perfect score: 616
Sequence: 1 MPSPGTVCSLLLGMLWLDL.........PPSSRERSRRSHQPSCSPEL 116

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop   6.0 , Delext 7.0

Searched: 32822875 seqs, 1821865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10659782/runat_05022005_161918_4281/app_query.fasta_1.263
-DB=EST -QFMT=fastp -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10659782 @CGN_1_3437 @runat_05022005_161918_4281 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   EST:*
               1: gb_est1:*
               2: gb_est2:*
               3: gb_htc:*
               4: gb_est3:*
               5: gb_est4:*
               6: gb_est5:*
               7: gb_est6:*
               8: gb_gss1:*
               9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	527.5	85.6	431	2	BF929001	BF929001 CM2-NT018
2	214	34.7	354	9	AY413163	AY413163 Homo sapi
3	214	34.7	526	4	BM854032	BM854032 K-EST0136
c 4	214	34.7	672	5	BM982194	BM982194 UI-CF-EN1
5	214	34.7	678	2	CA449820	CA449820 UI-H-EI1-
c 6	208.5	33.8	478	5	BX093784	BX093784 BX093784
7	207	33.6	334	9	AY413164	AY413164 Pan trogl
c 8	199.5	32.4	695	3	CE845760	CE845760 tigr-gss-
c 9	190	30.8	542	4	BI907288	BI907288 603063866
c 10	187	30.4	600	1	AA530994	nj07a01.s
11	178	28.9	523	6	BY708559	BY708559
12	178	28.9	528	3	AK008658	Mus muscu
13	178	28.9	528	3	AK008860	Mus muscu
14	173	28.1	581	7	CK373838	laie4d06.
15	173	28.1	587	7	CF424809	lad50f07.
16	172	27.9	415	4	BM022807	id62b10.y
17	172	27.9	415	4	BM054332	id55f03.y
18	172	27.6	458	7	CF581610	AGENCOURT
19	170	27.6	334	9	AY413165	Mus muscu
20	169	27.4	404	5	BY096920	BY096920
21	165	26.8	758	9	AG071477	Pan trogl
22	164.5	26.7	343	5	BY112615	BY112615
23	164.5	26.7	370	5	BY083794	BY083794
24	160	26.0	330	5	BY149645	BY149645
25	157	25.5	294	2	BF543543	UI-R-C3-t
26	152	24.7	289	2	BB564523	BB564523
c 27	149.5	24.3	449	1	AI138429	qq92a05.x
c 28	133.5	21.7	223	4	BI966558	id55f03.x
29	126	20.5	237	2	BB583439	BB583439
c 30	109	17.7	419	1	AI057396	ow75f03.x
c 31	106	17.2	558	7	CO055559	TgESTzyo6
c 32	104.5	17.0	635	9	CG311875	OGXCM40TV
c 33	104.5	17.0	667	9	CC636927	OGJBK53TV
c 34	104.5	17.0	813	9	CG338514	OG2BF65TH
c 35	104	16.9	494	9	CG455078	PUFXO84TD
c 36	103.5	16.8	885	4	BI227046	602952211
37	99	16.1	448	7	CN619603	TgESTzym8
38	99	16.1	517	4	BG657206	TgESTzya1
39	99	16.1	531	7	CK735827	TgESTzyk6
40	99	16.1	532	7	CK736563	TgESTzyk2
41	99	16.1	535	6	CB301576	TgESTzyf7
42	99	16.1	541	4	BG660654	TgESTzya1
43	99	16.1	545	4	BM188954	TgESTzyb4
44	99	16.1	546	4	BM132122	TgESTzyb0
45	99	16.1	550	7	CK736357	TgESTzyk2

ALIGNMENTS

RESULT 1
BF929001

LOCUS   BF929001   431 bp   mRNA   linear   EST 19-JAN-2001
DEFINITION CM2-NT0185-071200-586-a07 NT0185 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF929001
VERSION   BF929001.1 GI:12327129
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 431)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20202663
PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL

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(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM2&t2=CM2-NT0185-
071200-586-a07&t3=2000-12-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 431.
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source   1..431
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /dev_stage="Adult"
            /clone_lib="NT0185"
            /note"Organ: nervous tumor; Vector: puc18; Site_1: SmaI;
            Site_2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the pUC 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.:   8.98e-44   Length: 431
Score: 527.50   Matches: 101
Percent Similarity: 99.02%   Conservative: 0
Best Local Similarity: 99.02%   Mismatches: 0
Query Match: 85.63%   Indels: 1
DB: Gaps: 2

US-10-659-782A-32 (1-116) x BF929001 (1-431)

Qy   16 LeuTrpLeuAspLeuAlaMetAlaGlySerPheLeuSerProGluHisGlnArgVal 35
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Db   9 CTCTGGCTGGACTTGGCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAGCACCAGAGAGTC 68

Qy   36 GlnValArgProHisLysAlaProHisValValProAlaLeuProLeuSerAsnGln 55
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   69 CAGGTGAGACCTCCCCACAAAGCCCCACATGTGTTCCAGCCCCTGCCACTTAGCAACCAG 128

Qy   56 LeuCysAspLeuGluGlnArgHis---TrpAlaSerValPheSerGlnSerThrLys 74
         ||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db 129 CTCTGTGACCTGGAGCAGCAGCGCCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAG 188

Qy   75 AspSerGlySerAspLeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArg 94
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Db 189 GACTCCTGGGTCTGGATCTGACCTGTTTTCTGGAAGGACATGGGGGGCTTAGAGTCCTAAACAGA 248

Qy   95 LeuPheProSerProSerArgGluArgArgSerHisGlnProSerCysSerPro 114
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Db 249 CTGTTTCCCCCTTCCAGCAGGGAAAGGAGTCGAAGAAGCCACCAGCTGCAGCCCC 308

Qy 115 GluLeu 116
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Db 309 GAGCTC 314

RESULT 2
AY413163
LOCUS   AY413163   354 bp   DNA   linear   GSS 12-DEC-2003
DEFINITION   Homo sapiens HCM4799 gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION   AY413163
VERSION   AY413163.1 GI:39769128
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 354)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
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JOURNAL   gene trios
PUBMED   Science 302 (5552), 1960-1963 (2003)
REFERENCE   14671302
AUTHORS   2 (bases 1 to 354)
             Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
             Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
             them based on alignment.

FEATURES   Location/Qualifiers
source   1..354
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
gene   <1..>354
             /locus_tag="HCM4799"

ORIGIN

Alignment Scores:
Pred. No.:   6.65e-12   Length: 354
Score: 214.00   Matches: 51
Percent Similarity: 44.44%   Conservative: 1
Best Local Similarity: 43.59%   Mismatches: 0
Query Match: 34.74%   Indels: 65
DB: Gaps: 9

US-10-659-782A-32 (1-116) x AY413163 (1-354)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
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Qy   21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG------------ 108

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60

Db 108 -- 108

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80

Db 108 -- 108

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100

Db 108 -- 108

Qy 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
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Db 109 CAGAGAAAGGAGTCGAAGAAGAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 157

RESULT 3
BM854032
LOCUS   BM854032   526 bp   mRNA   linear   EST 06-MAR-2002
DEFINITION   K-EST0116326 S14K402 S14K402 Homo sapiens cDNA clone S14K402-37-H03 5',
             mRNA sequence.
ACCESSION   BM854032
VERSION   BM854032.1 GI:19210431
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 526)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
             Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
             Kim,Y.S.
  TITLE   21C Frontier Korean EST Project 2001

```
JOURNAL      Unpublished (2002)
COMMENT      Contact: Kim YS
             Genome Research Center
             Korea Research Institute of Bioscience & Biotechnology
             52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
             Tel: +82-42-860-4470
             Fax: +82-42-860-4409
             Email: yongsung@mail.kribb.re.kr
             Plate: 37  row: H  column: 03
             High quality sequence stop: 526.
FEATURES             Location/Qualifiers
     source          1..526
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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                     /cell_line="K402"
                     /lab_host="Top10F'"
                     /clone_lib="S14K402"
                     /note="Organ: Stomach; Vector: pT218RP1; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."

ORIGIN

Alignment Scores:
Pred. No.:           1.13e-11        Length:           526
Score:               214.00          Matches:          51
Percent Similarity:  44.44%          Conservative:     1
Best Local Similarity: 43.59%        Mismatches:       0
Query Match:         34.74%          Indels:           65
DB:                                  Gaps:             4

US-10-659-782A-32 (1-116) x BM854032 (1-526)

Qy    1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
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Db   50 ATGCCCTCCCCAGGGACCGTGTGCAGCCTCCTGCTCCTCCGGATGCTCTGGCTGGACTTG 109

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
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Db  110 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG------------ 157

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuProLeuCysAspLeuGlu 60
Db  157 ------------------------------------------------------------ 157

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db  157 ------------------------------------------------------------ 157

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 100
Db  157 ------------------------------------------------------------ 157

Qy  101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
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Db  158 CAGAGAAAGGAGTCGAAGAAGCCACCAAGCTCCAGCCCCGACCTC 206

RESULT 4
BM982194/c
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LOCUS       BM982194       672 bp    mRNA       linear   EST 21-FEB-2003
DEFINITION  UI-CF-EN1-acr-k-05-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
            UI-CF-EN1-acr-k-05-0-UI 3', mRNA sequence.
ACCESSION   BM982194
VERSION     BM982194.1  GI:19605448
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 672)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..672
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EN1-acr-k-05-0-UI"
                     /tissue_type="Primary Lung Cystic Fibrosis Epithelial
                     Cells"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EN1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EN1 is a normalized cDNA library containing the
                     following tissue(s): Primary Lung Cystic Fibrosis
                     Epithelial Cells. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site. Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I, and cloned directionally into pT7T3-Pac vector. The
                     oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CTGCTCAGGT.
                     TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
                     6hr to LPS 24h
                     TAG_LIB=UI-CF-EN1
                     TAG_SEQ=CTGCTCAGGT"
ORIGIN

Alignment Scores:
Pred. No.:           1.58e-11        Length:           672
Score:               214.00          Matches:          51
Percent Similarity:  44.44%          Conservative:     1
Best Local Similarity: 43.59%        Mismatches:       0
Query Match:         34.74%          Indels:           65
DB:                                  Gaps:             1

US-10-659-782A-32 (1-116) x BM982194 (1-672)
```

```
Qy    1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
        ||||||||||||||||||||||||||||||||||||||||||||
Db  496 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCAGCCTCCTCCTGGCATGCTCTGGCTGGACTTG 437

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
        |||||||||||||||||||||||||||||||
Db  436 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG---------- 389

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnLeuCysAspLeuGlu 60
Db  389 ---------------------------------------------- 389

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db  389 ---------------------------------------------- 389

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db  389 ---------------------------------------------- 389

Qy  101 Arg-GluArgArgArgSerHisSerGlnProSerCysSerProGluLeu 116
        :::  |||||||||||||||||||||||||||||||||
Db  388 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 340

RESULT 5
CA449820/c
LOCUS       CA449820               678 bp    mRNA    linear   EST 08-NOV-2002
DEFINITION  UI-H-EI1-ayy-c-12-0-UI.s1 NCI_CGAP_EI1 Homo sapiens cDNA clone
            UI-H-EI1-ayy-c-12-0-UI 3', mRNA sequence.
ACCESSION   CA449820
VERSION     CA449820.1   GI:24814240
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 678)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..678
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EI1-ayy-c-12-0-UI"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_EI1"
                     /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
                     NCI_CGAP_EI1 is a normalized cDNA library containing the
                     following tissue(s): Chondrosarcoma. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     ACACTTGCAC.
                     TAG_TISSUE=chondrosarcoma
                     TAG_LIB=UI-H-EI1
                     TAG_SEQ=ACACTTGCAC"
ORIGIN

Alignment Scores:
Pred. No.:                 1.6e-11       Length:          678
Score:                     214.00        Matches:         51
Percent Similarity:        44.44%        Conservative:    1
Best Local Similarity:     43.59%        Mismatches:      0
Query Match:               34.74%        Indels:          65
DB:                                      Gaps:            1

US-10-659-782A-32 (1-116) x CA449820 (1-678)

Qy    1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
        ||||||||||||||||||||||||||||||||||||||||||||
Db  496 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCAGCCTCCTCCTGGCATGCTCTGGCTGGACTTG 437

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
        |||||||||||||||||||||||||||||||
Db  436 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG---------- 389

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnLeuCysAspLeuGlu 60
Db  389 ---------------------------------------------- 389

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db  389 ---------------------------------------------- 389

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db  389 ---------------------------------------------- 389

Qy  101 Arg-GluArgArgArgSerHisSerGlnProSerCysSerProGluLeu 116
        :::  |||||||||||||||||||||||||||||||||||
Db  388 CAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTC 340

RESULT 6
BX093784
LOCUS       BX093784               478 bp    mRNA    linear   EST 04-FEB-2003
DEFINITION  BX093784 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
            IMAGp998E094758 ; IMAGE:1938800, mRNA sequence.
ACCESSION   BX093784
VERSION     BX093784.1   GI:27841729
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 478)
AUTHORS     Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
            Radelof,U., Schneider,D. and Korn,B.
TITLE       Human UnigeneSet - RZPD3
JOURNAL     Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998E094758.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Human UnigeneSet - RZPD3 (RZPDLIB No.972)
            http://www.rzpd.de/cgi-
            bin/showLib.pl.cgi/response?libNo=972  Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
```

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            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES        Location/Qualifiers
source          1..478
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGp998E094758 ; IMAGE:1938800"
                /dev_stage="8-9 weeks"
                /lab_host="DH10B"
                /clone_lib="Soares_total_fetus_Nb2HF8_9w"
                /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                was prepared from mRNA obtained from pooled 8-9 week
                (total) fetus material with a Not I - oligo(dT) primer [5'
                TGTTACCAATCTGAAGTGGAGCGGCCGCCGTTAATTTTTTTTTTTTTTTT 3'].
                Double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT7T3 vector. Library
                went through one round of normalization, and was
                constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

Alignment Scores:
Pred. No.:              3.63e-11         Length:        478
Score:                  208.50           Matches:       50
Percent Similarity:     43.59%           Conservative:  1
Best Local Similarity:  42.74%           Mismatches:    0
Query Match:            33.85%           Indels:        66
DB:                     5                Gaps:          1

US-10-659-782A-32 (1-116) x BX093784 (1-478)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu  20
        ||||||||||||||||||||||||||||||||||||
Db  33 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCCATGCTGGCTGGACTTG  92

Qy  21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro  40
        ||||||||||||||||||||||||||||||||||||
Db  93 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGTC--------------  137

Qy  41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu  60
Db 137 ------------------------------------------------------------- 137

Qy  61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysSerGlySerAspLeu  80
Db 137 ------------------------------------------------------------- 137

Qy  81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db 137 ------------------------------------------------------------- 137

Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
        ||||||||||||||||||||||||||||||||||||||||||
Db 138 CAGAGAAAGGAGTCGAAGAGCCACCAGCCACCAAGCTGCAGCCCCGAGCTC 186

RESULT 7
AY413164
LOCUS       AY413164       334 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Pan troglodytes HCM4799 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY413164
VERSION     AY413164.1  GI:39769129
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM    Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 334)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
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            Adams,M.D. and Cargill,M.
TITLE       Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL     Science 302 (5652), 1960-1963 (2003)
PUBMED      14671302
REFERENCE   2  (bases 1 to 334)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES        Location/Qualifiers
source          1..334
                /organism="Pan troglodytes"
                /mol_type="genomic DNA"
                /db_xref="taxon:9598"
gene            <1..>334
                /locus_tag="HCM4799"
ORIGIN

Alignment Scores:
Pred. No.:              3.19e-11         Length:        334
Score:                  207.00           Matches:       50
Percent Similarity:     43.59%           Conservative:  1
Best Local Similarity:  42.74%           Mismatches:    1
Query Match:            33.60%           Indels:        65
DB:                     9                Gaps:          1

US-10-659-782A-32 (1-116) x AY413164 (1-334)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu  20
        |||||||||||||||||||||||||||||||
Db   1 ATGCCCTCCCCCNNNGACCGTCTGCAGCCTCCTGCTCCTCGGCCATGCTGGCTGGACTTG  60

Qy  21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro  40
        ||||||||||||||||||||||||||||||||||||
Db  61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGTCCAG------------- 108

Qy  41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu  60
Db 108 ------------------------------------------------------------- 108

Qy  61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysSerGlySerAspLeu  80
Db 108 ------------------------------------------------------------- 108

Qy  81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db 108 ------------------------------------------------------------- 108

Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
        :::  |||||||||||||||||||||||||||||||||||||||||
Db 109 CAGAGAAAGGAGTCGAAGAGCCACCAGCCACCAAGCTGCAGCCCCGAGCTC 157

RESULT 8
CE845760/c
LOCUS       CE845760       695 bp    DNA     linear   GSS 01-OCT-2003
DEFINITION  tigr-gss-dog-1700033274I330 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE845760
VERSION     CE845760.1  GI:37208555
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
ORGANISM    Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 695)
AUTHORS     Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
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TITLE   Venter,J.C.
JOURNAL   The dog genome: survey sequencing and comparative analysis
          Science 301 (5641), 1898-1903 (2003)
MEDLINE   22875432
PUBMED   14512627
COMMENT   Contact: Kirkness EF
          The Institute for Genomic Research
          Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
          Rockville, MD 20850, USA
          Tel: 301-838-0200
          Fax: 301-838-0208
          Email: ekirknes@tigr.org
          Class: shotgun.
FEATURES   Location/Qualifiers
     source   1..695
                   /organism="Canis familiaris"
                   /mol_type="genomic DNA"
                   /strain="Standard Poodle"
                   /db_xref="taxon:9615"
                   /clone_lib="Dog Library"
                   /note="Site 1: BstXI; Libraries were prepared from
                   peripheral Blood"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 4.97e-10   Length: 695
Percent Similarity: 199.50   Matches: 66
Best Local Similarity: 67.89%   Conservative: 8
Query Match: 60.55%   Mismatches: 20
DB: 32.39%   Indels: 19
                                        Gaps: 6

US-10-659-782A-32 (1-116) x CE845760 (1-695)

Qy   19 AspLeuAlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArg 38
        ||||||||||||||||||||| :::::||||||
Db 695 GACCTGGCCATGGCAGGGGGCTCCAGCTTCCTAAGTCCGAACACCAGAAACTACAGGTAAA- 637

Qy   39 Pro---ProHisLysAlaProHis-------------ValValProAlaLeuProLeu 52
        ||| ||||||||||||| :::|||
Db 636 CCATCTCCCCACACAAAGCCCCACG-TTTGGATTAGGGTATCTGGCTCCAGCCTTGCCATCG 578

Qy   53 SerAsnGlnLeuCysAspGluGluGlnGlnArgHisTrpAlaSerValPheSerGlnSer 72
        ::|||||||||||||| ||||::::
Db 577 GGCAGCCAGCTGTGTGACCTTG--GCTCAAATTCTCTGGCT-----TTCTCCAAGAGC 526

Qy   73 Thrlys---AspSerGlySerAspLeu---------ThrValSerGlyArgThr 86
        ||||| |||||||||| ::: ||||||
Db 525 ACTAAGGACGACTCTGGGTCTGACTGTAGGCTCCACCCCCTGCTTCTGGAAGTATA 466

Qy   87 TrpGlyLeuArgLeuAsnArgLeuPheProProSerProSerArgGluArgSerArgArg 106
        |||||||||||||||
Db 465 AGGGGGCTTAGGGCCCTA--AGATA-GTACCTCTTTCCAGCAGCAGAAAAGGAGTCCAAGA 410

Qy 107 SerHisGlnProSerCysSerProGlu 115
        ||| ::::|||||||
Db 409 AGCCGCCGGCCAAACTGCAGCCCCGAG 383

RESULT 9
BI907288
LOCUS   BI907288   542 bp   mRNA   linear   EST 16-OCT-2001
DEFINITION 603063866F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212768 5',
            mRNA sequence.
ACCESSION   BI907288
VERSION   BI907288.1 GI:16170099
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 542)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11534 row: d column: 17
            High quality sequence stop: 535.
FEATURES   Location/Qualifiers
     source   1..542
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:5212768"
                   /tissue_type="leukocyte"
                   /lab_host="DH10B"
                   /clone_lib="NIH_MGC_118"
                   /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
                   (destroyed); RNA source leukocytes from anonymous pool of
                   non-activated adult donors. Library is oligo-dT primed
                   and directionally cloned (EcoRV site is destroyed upon
                   cloning). Average insert size 1.7 kb insert size range
                   1.2-3.3 kb. Library is normalized and enriched for
                   full-length clones and was constructed by C. Gruber
                   (Invitrogen). Research Genetics tracking code 027. Note:
                   this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:
Score: 3.32e-09   Length: 542
Percent Similarity: 190.00   Matches: 50
Best Local Similarity: 43.59%   Conservative: 1
Query Match: 42.74%   Mismatches: 1
DB: 30.84%   Indels: 66
                                        Gaps: 1

US-10-659-782A-32 (1-116) x BI907288 (1-542)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
        |||||||||||
Db   40 ATGCCCTCCCCAGGGACC-GTCTGCAGCCTCCTGCTCCTCCTGGGCATGCTCTGGCTGGACTTG 98

Qy   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
        |||||||||||||||||||||||||||||||||||
Db   99 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG---------- 146

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 146 ------ 146

Qy   61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 146 ------ 146

Qy   81 ThrValSerGlyArgThrTrpGlyLeuArgLeuAsnArgLeuPheProProSer 100
Db 146 ------ 146

Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
        ::: |||||||||||||
Db 147 CAGAGAAGGAGTCGAAGAAGCACCAGCCACCAAGCTGCAGCCCGAGCTC 195

RESULT 10
AA530994
AA530994/c
LOCUS   AA530994   600 bp   mRNA   linear   EST 20-AUG-1997
DEFINITION nj07a01.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:985608 3',
            mRNA sequence.
ACCESSION   AA530994
VERSION   AA530994.1 GI:2273700

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Qy      104 SerArgArgSerHisGlnProSerCysSerProGluLeu 116
            ||||||||||||||||||||||||||||||||||||||
Db      376 AGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCGAGCTC 338
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RESULT 11
BY708559
LOCUS       BY708559          523 bp  mRNA      linear       EST 16-DEC-2002
DEFINITION  BY708559 RIKEN full-length enriched, adult male stomach Mus
            musculus cDNA clone 2210006E23 5', mRNA sequence.
ACCESSION   BY708559
VERSION     BY708559.1  GI:27119750
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   MEDLINE  22354683
   PUBMED   12466851
  COMMENT   Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
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            Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,H.,
            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
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KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement:Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1417   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 314.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:985608"
                     /sex="male"
                     /tissue_type="normal prostate"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Pr22"
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                     with a modified polylinker; 1st strand cDNA was prepared
                     from normal prostate bulk tissue, and was then primed with
                     a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library is normalized, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN
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Pred. No.:            7.69e-09
Score:             187.00
Percent Similarity:  42.48%           Length:          600
Best Local Similarity: 40.71%         Matches:          46
Query Match:         30.36%           Conservative:      2
DB:                                   Mismatches:        1
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Db   484 CCAAGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCA 425

Qy    24 GlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProProHisLysAla 43
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Db   424 GGCTCCAGCTTCCTGAGCCCTGAA------------------------------------ 401

Qy    44 ProHisValValProAlaLeuProLeuSerArgAsnGlnLeuCysAspLeuGluGlnGlnArg 63
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Db   401 ----------------------------------------------------------- 401

Qy    64 HisTrpAlaSerValPheSerGlnSerThrLysAspAspSerGlySerAspLeuThrValSer 83
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Db   400 --------------------------ACCAGAGAG------------------------ 392

Qy    84 GlyArgThrGlyTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSerArgGluArg 103
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Db   391 -----------------------------------------TCCAGCAGAGAGAAAGG 377
```

```
                    Computer-based methods for the mouse full-length cDNA
                    encyclopedia: real-time sequence clustering for construction of a
                    nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
                    cDNA library was prepared and sequenced in Mouse Genome
                    Encyclopedia Project of Genome Exploration Research Group in Riken
                    Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                    Division of Experimental Animal Research in Riken contributed to
                    prepare mouse tissues.
                    Please visit our web site (http://genome.gsc.riken.go.jp) for
                    further details.
FEATURES            Location/Qualifiers
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                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /clone="2210006E23"
                    /sex="male"
                    /tissue_type="stomach"
                    /dev_stage="adult"
                    /lab_host="SOLR"
                    /clone_lib="RIKEN full-length enriched, adult male
                    stomach"
                    /note="Site 1: XhoI; Site 2: SstI; cDNA library was
                    prepared and sequenced in Mouse Genome Encyclopedia
                    Project of Genome Exploration Research Group in Riken
                    Genomic Sciences Center and Genome Science Laboratory in
                    RIKEN. Division of Experimental Animal Research in Riken
                    contributed to prepare mouse tissues. 1st strand cDNA was
                    primed with a primer [5'
                    GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTTVN 3'], cDNA was
                    prepared by using trehalose thermo-activated reverse
                    transcriptase and subsequently enriched for full-length by
                    cap-trapper. Second strand cDNA was prepared with the
                    primer adapter of sequence [5'
                    GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA
                    was cleaved with XhoI and SstI."
ORIGIN
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Alignment Scores:
Pred. No.:              .523
Score:                  5.3e-08          Length:              523
Percent Similarity:     178.00           Matches:             54
Best Local Similarity:  45.71%           Conservative:        10
Query Match:            38.57%           Mismatches:          39
DB:                     28.90%           Indels:              37
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US-10-659-782A-32 (1-116) x BY708559 (1-523)
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Qy     21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnArgValArgProPro 40
          |||||||||||||||||||||||||||||:|:  ||| |||
Db    100 GCCATGGCAGGCTCCAGCTTCCTGAGCCCAGAGCACCAGAAGCCCAGCAGGAAAGGAA 159

Qy     41 HisLysAlaProHisValValProAlaLeuProLeuSerArgAsnGlnLeuCysAspLeuGlu 60
          ||                                     |||
Db    160 TCCAAGAAGCCA----------------------CCAGCTAAACTGCAGCCACCAGAGCTCTGGAA 201

Qy     61 GlnGlnArgHis----------------------------------------- 64
          |||
Db    202 GGCTGCTGGCTCCACCCAGAGGACAGAGGACAAGCAGAGAAGAGACAGAGGAGAGCTGGAGATC 261

Qy     65 ---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspGlySerAspLeuThrValSer 83
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Qy     84 GlyArgThrTrpGlyValLeuArgValLeuAsnArgLeuPheProProSerSerArgGluArg 103
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DEFINITION       Mus musculus adult male stomach cDNA, RIKEN full-length enriched
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                 sequence.
ACCESSION        AK008658
VERSION          AK008658.1  GI:12842985
KEYWORDS         HTC; CAP trapper.
SOURCE           Mus musculus (house mouse)
  ORGANISM       Mus musculus
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE        1
  AUTHORS        Carninci,P. and Hayashizaki,Y.
  TITLE          High-efficiency full-length cDNA cloning
  JOURNAL        Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE        99279253
   PUBMED        10349636
REFERENCE        2
  AUTHORS        Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
                 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE          Normalization and subtraction of cap-trapper-selected cDNAs to
                 prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL        Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE        20499374
   PUBMED        11042159
REFERENCE        3
  AUTHORS        Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
                 Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
                 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
                 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
                 Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,J.,
                 Yoneda,Y., Ishikawa,T., Ozawa,S., Tanaka,T., Matsuura,S., Kawai,J.,
                 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE          RIKEN integrated sequence analysis (RISA) system-384-format
                 sequencing pipeline with 384 multicapillary sequencer
  JOURNAL        Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE        20530913
   PUBMED        11076881
REFERENCE        4
  AUTHORS        The RIKEN Genome Exploration Research Group Phase II Team and the
                 FANTOM Consortium.
  TITLE          Functional annotation of a full-length mouse cDNA collection
  JOURNAL        Nature 409, 685-690 (2001)
REFERENCE        5
  AUTHORS        The FANTOM Consortium and the RIKEN Genome Exploration Research
                 Group Phase I & II Team.
  TITLE          Analysis of the mouse transcriptome based on functional annotation
                 of 60,770 full-length cDNAs
  JOURNAL        Nature 420, 563-573 (2002)
REFERENCE        6  (bases 1 to 527)
  AUTHORS        Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
                 Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
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                 Tejima,Y., Toya,T., Yamamura,Y., Yasunishi,A., Yoshida,K.,
                 Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE          Direct Submission
  JOURNAL        Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                 Physical and Chemical Research (RIKEN), Laboratory for Genome
                 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
                 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp),
```

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Db

Qy

Db

Qy

Db
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RESULT 13
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DEFINITION   Mus musculus adult male stomach cDNA, RIKEN full-length enriched
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               sequence.
ACCESSION   AK008860
VERSION   AK008860.1   GI:12843305
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE   High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
MEDLINE   99279253
PUBMED   10049636
REFERENCE   2
AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
               Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
               prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   20499374
PUBMED   11042159
REFERENCE   3
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
               Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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               Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
               Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
               sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE   20530913
PUBMED   11076861
REFERENCE   4
AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
               FANTOM Consortium.
TITLE   Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
               Group Phase I & II Team.
TITLE   Analysis of the mouse transcriptome based on functional annotation
               of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6   (bases 1 to 528)
AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
               Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
               Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
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               Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
               Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
               Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
               Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
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Db

Qy

Db

Qy

Db
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COMMENT   URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
               Fax:81-45-503-9216)
               Please visit our web site (http://genome.gsc.riken.jp/) for further
               details.
               cDNA library was prepared and sequenced in Mouse Genome
               Encyclopedia Project of Genome Exploration Research Group in Riken
               Genomic Sciences Center and Genome Science Laboratory in RIKEN.
               Division of Experimental Animal Research in Riken contributed to
               prepare mouse tissues. First strand cDNA was primed with a primer
               [5' GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
               prepared by using trehalose thermo-activated reverse transcriptase
               and subsequently enriched for full-length by cap-trapper. Second
               strand cDNA was prepared with the primer adapter of sequence [5'
               GAGAGAGAGATTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3'], cDNA was cleaved
               with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
               Host: SOLR.

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               /tissue_type="stomach"
               /clone_lib="RIKEN full-length enriched mouse cDNA library"
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               QDILWEEVKEAPADK"

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ORIGIN

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Pred. No.:   5.35e-08   Length: 527
Score: 178.00   Matches: 54
Percent Similarity: 45.71%   Conservative: 10
Best Local Similarity: 38.57%   Mismatches: 39
Query Match: 28.90%   Indels: 37
DB: 3   Gaps: 5
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US-10-659-782A-32 (1-116) x AK008658 (1-527)

Qy     1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
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Db    44 ATGTCTGTCTTCAGGACCACCATCTGCAGTTTGCTGCTACTCAGCATGCTCTGGATGGACATG 103

Qy    21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnArgValArgProPro 40
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Qy    41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
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Qy    65 ---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeuThrValSer 83
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TITLE
JOURNAL   Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
           Direct Submission
           Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
           Physical and Chemical Research (RIKEN), Laboratory for Genome
           Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
           RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
           Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
           URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
           Fax:81-45-503-9216)
COMMENT   Please visit our web site (http://genome.gsc.riken.jp/) for further
           details.
           cDNA library was prepared and sequenced in Mouse Genome
           Encyclopedia Project of Genome Exploration Research Group in Riken
           Genomic Sciences Center and Genome Science Laboratory in RIKEN.
           Division of Experimental Animal Research in Riken contributed to
           prepare mouse tissues. First strand cDNA was primed with a primer
           [5' GAGAGAGAAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTTVN 3'], cDNA was
           prepared by using trehalose thermo-activated reverse transcriptase
           and subsequently enriched for full-length by cap-trapper. Second
           strand cDNA was prepared with the primer adapter of sequence [5'
           GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
           with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
           Host: SOLR.
FEATURES   Location/Qualifiers
     source   1..528
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:2210408M22"
                     /db_xref="taxon:10090"
                     /clone="2210408M22"
                     /sex="male"
                     /tissue_type="stomach"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS   44..397
                     /note="unnamed protein product; GHRELIN PRECURSOR
                     (SWISSPROT|Q9EQX0, evidence: FASTY, 100%ID, 100%length,
                     match=351)
                     putative"
                     /codon_start=1
                     /protein_id="BAB25934.1"
                     /db_xref="GI:12843306"
                     /translation="MLSSGTICSLLLLSMLWMDMAMAGSSFLSPEHQKAQQRKESKKP
                     PAKLQPRALEGWLHPEDRGQAEBTEELEIRFNAPFFDVGIKLSGAQYQQHGRALGKPL
                     QDILWEEVKEAPADK"
     polyA_signal   499..504
                     /note="putative"
     polyA_site   528
                     /note="putative"
ORIGIN

Alignment Scores:
Pred. No.:   5.36e-08
Score: 178.00
Percent Similarity: 45.71%
Best Local Similarity: 38.57%
Query Match: 28.90%
DB: 3

US-10-659-782A-32 (1-116) x AK008860 (1-528)

Qy   1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
         ||||||||||||||||||||||||||||||||:||:|||||||||||:||:||
Db   44 ATGCTGTCTTCAGGCACCATCTGCAGTTTGCTGCTACTCAGCATGCTCTGGATGGACATG 103

Qy   21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
         |||||||||||||||||||||||||||||||||||||:|::|||||
Db   104 GCCATGGCAGGCTCCAGCTTCCTGAGCCCAGAGCACCAGAAAGCCAGCAGAGAAGGAA 163

Qy   41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
         ||| ||| |||
Db   164 TCCCAAGAAGCCA--------------------CCAGCTAAACTGCAGCCACGAGCTCTGGAA 205

                                                                          64
     61 GlnGlnArgHis--------------------------------------
         |||
    206 GGCTGGCTCCACCCAGGACAGGACAGCAGCAGAGACAGAGAGCTGAGATC 265

     65 ---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerLeuThrValSer 83
         |:| ::: ||||||||||:::
    266 AGGTTCAATGTCCCCTTCGATGTTGGCATCAAGTGTCAGGAGCTCAGTATCAGCAGCAT 325

     84 GlyArgThr-TrpGlyLeuArgValLeuAsnArgLeuPheProProSerArgGluAr 103
         ||||||| ||| :::||
    326 GGCCGGGCCCTGGGA--------------------AGTTTCTTCAGGATATCCTCTGGGAAGAG 370

    103 gSerArgArg----------------SerHisGln--------ProSerCysSerPro 114
         ||||:::||| :::||
    371 GTCAAAGAGGCGCCAGCTGACAAGTAACCACGGACAGGCCTGACCCCCGTGCTTTCCT 428

RESULT 14
CK373838
LOCUS   CK373838   581 bp   mRNA   linear   EST 23-DEC-2003
DEFINITION   1ai64d06.y1 Gastric Epithelial Progenitor 2 Mus musculus cDNA 5'
                similar to TR:Q9QYH7 Q9QYH7 GHRELIN PRECURSOR. ;, mRNA sequence.
ACCESSION   CK373838
VERSION   CK373838.1   GI:40339080
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 581)
  AUTHORS   Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J.,
                Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J.,
                Ronko,I., Tsagareishvili,R., Belaygorod,L., Grow,A., Maguire,L.,
                Waterston,R. and Wilson,R.
  TITLE   WashU Stem cell EST Project
  JOURNAL   Unpublished (2002)
COMMENT   Contact: Jeff Gordon and Mike Lovett
                WashU, Human Genetics Division
                Washington University School of Medicine
                1st strand of cDNA was synthesized with reverse transcriptase and
                oligo(dT) beads, then cDNA was amplified by PCR using modified
                SMART primers. The final cDNA was cloned in pAMP1 vector in
                annealing reaction with Uracil DNA Glycosylase (UDG). Library
                constructed by Y.Korshunova and M. Lovett. Library materials
                provided by Mills JC & Gordon JI.
                Seq primer: -40RP from Gibco.
FEATURES   Location/Qualifiers
     source   1..581
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="Laser-captured isthmal cells from tox176
                     transgenic mice"
                     /dev_stage="adult"
                     /lab_host="DH5alpha"
                     /clone_lib="Gastric Epithelial Progenitor 2"
                     /note="vector: pAMP1; 1st strand of cDNA was synthesized
                     with reverse transcriptase and oligo(dT) beads, then cDNA
                     was amplified by PCR using modified SMART primers. The
                     final cDNA was cloned in pAMP1 vector in annealing
                     reaction with Uracil DNA Glycosylase (UDG). Library
                     constructed by Y.Korshunova and M. Lovett. Library
                     materials provided by Mills JC & Gordon JI."
ORIGIN

Alignment Scores:
Pred. No.:   1.98e-07   Length: 581
Score: 173.00   Matches: 49
Percent Similarity: 47.54%   Conservative: 9
Best Local Similarity: 40.16%   Mismatches: 35
Query Match: 28.08%   Indels: 29
DB: Gaps: 3

cloned in pAMP1 vector in annealing reaction with Uracil
DNA Glycosylase (UDG). Library constructed by Y.Korshunova
and M. Lovett. Library materials provided by Mills JC &
Gordon JI."

ORIGIN

Alignment Scores:
Pred. No.:   2e-07   Length: 587
Score: 173.00   Matches: 49
Percent Similarity: 47.54%   Conservative: 9
Best Local Similarity: 40.16%   Mismatches: 35
Query Match: 28.08%   Indels: 29
DB: 7   Gaps: 3

US-10-659-782A-32 (1-116) x CF424809 (1-587)

Qy   3 SerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeuAlaMet 22
         ||| |||:::||||||||||||||||||:::||:||||||
Db   220 TCTTCAGGCACCATCTGCAGTTGCTGCTACTCAGCATGCTGGATGGACATGGCCATG 279

Qy   23 AlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProProHisLys 42
         |||||||||||||||||||||::: ||| |||
Db   280 GCAGGCTCCAGCTTCCTGAGCCCAGAGCACCAGAAAGCCCAGAGAGAAAGGAATCCAAG 339

Qy   43 AlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGluGlnGln 62
         ||||| |||||| |||||||
Db   340 AAGCCA------------------CCAGCTAAACTGCAGCCCACGAGCTCTGGAAGGCTGG 381

Qy   63 ArgHis-------------------------Trp 65
         || :::
Db   382 CTCCACCCAGAGGACAGAGGACAAGCAGCAGAAGAGACAGGAGGAGGAGCTGGAGATCAGTTC 441

Qy   66 AlaSerValPheSerGlnThrLysAspLeuThrValSerGlyArg 85
         ::: |||||||||||||||||||||:::
Db   442 AATGCTCCCTTCGATGTTGGCATCAAGCTGTCAGTATCAGCATGGCCGG 501

Qy   86 Thr-TrpGlyLeuArgValLeuAsnArgLeuPheProProSerSerArgGluArgSerAr 105
         ||||| :::||||||
Db   502 GCCCTGGGGA-----------------AGTTTCTTCAGGATATCCTCTGGAAGAGGTCAAA 546

Qy   105 gArg 106
         :|||
Db   547 GAGG 550

Search completed: February 10, 2005, 15:59:45
Job time : 2555 secs

US-10-659-782A-32 (1-116) x CK373838 (1-581)

Qy   3 SerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeuAlaMet 22
         ||| |||:::||||||||||||||||||:::||:||||||
Db   220 TCTTCAGGCACCATCTGCAGTTGCTGCTACTCAGCATGCTGGATGGACATGGCCATG 279

Qy   23 AlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProProHisLys 42
         |||||||||||||||||||||::: ||| |||
Db   280 GCAGGCTCCAGCTTCCTGAGCCCAGAGCACCAGAAAGCCCAGAGAGAAAGGAATCCAAG 339

Qy   43 AlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGluGlnGln 62
         ||||| |||||| |||||||
Db   340 AAGCCA------------------CCAGCTAAACTGCAGCCCACGAGCTCTGGAAGGCTGG 381

Qy   63 ArgHis-------------------------Trp 65
         || :::
Db   382 CTCCACCCAGAGGACAGAGGACAAGCAGCAGAAGAGACAGGAGGAGGAGCTGGAGATCAGTTC 441

Qy   66 AlaSerValPheSerGlnThrLysAspLeuThrValSerGlyArg 85
         ::: |||||||||||||||||||||:::
Db   442 AATGCTCCCTTCGATGTTGGCATCAAGCTGTCAGTATCAGCATGGCCGG 501

Qy   86 Thr-TrpGlyLeuArgValLeuAsnArgLeuPheProProSerSerArgGluArgSerAr 105
         ||||| :::||||||
Db   502 GCCCTGGGGA-----------------AGTTTCTTCAGGATATCCTCTGGAAGAGGTCAAA 546

Qy   105 gArg 106
         :|||
Db   547 GAGG 550

RESULT 15
CF424809
LOCUS   CF424809   587 bp   mRNA   linear   EST 03-SEP-2003
DEFINITION 1ad50f07.y1 Gastric Epithelial Progenitor Mus musculus cDNA 5'
            similar to TR:Q9QYH7 Q9QYH7 GHRELIN PRECURSOR. ;, mRNA sequence.
ACCESSION   CF424809
VERSION   CF424809.1 GI:34437510
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 587)
  AUTHORS   Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J.,
            Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J.,
            Ronko,I., Tsagareishvili,R., Belaygorod,L., Grow,A., Maguire,L.,
            Waterston,R. and Wilson,R.
  TITLE   WashU Stem cell EST Project
  JOURNAL   Unpublished (2002)
  COMMENT   Contact: Jeff Gordon and Mike Lovett
            WashU, Human Genetics Division
            Washington University School of Medicine
            1st strand of cDNA was synthesized with reverse transcriptase and
            oligo(dT) beads, then cDNA was amplified by PCR using modified
            SMART primers. The final cDNA was cloned in pAMP1 vector in
            annealing reaction with Uracil DNA Glycosylase (UDG). Library
            constructed by Y.Korshunova and M. Lovett. Library materials
            provided by Mills JC & Gordon JI.
            Seq primer: -40RP from Gibco.
FEATURES   Location/Qualifiers
     source   1..587
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="Gastric Epithelial Progenitor"
                     /dev_stage="adult"
                     /lab_host="DH5alpha"
                     /clone_lib="Gastric Epithelial Progenitor"
                     /note="Vector: pAMP1; This library was created from
                     laser-captured isthmal cells from tox176 transgenic mice.
                     1st strand of cDNA was synthesized with reverse
                     transcriptase and oligo(dT) beads, then cDNA was amplified
                     by PCR using modified SMART primers. The final cDNA was